STIC-Biotech/ChemLib

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From:

Rao, Manjunath N.

Sent:

Wednesday, August 14, 2002 12:47 PM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search request for 10/003,759

From: Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10C 01

Phone: 306-5681

Date: 8-14-02

Please search the following as soon as possible for application with serial number 10/003,759

SEQ ID NO: 1, SEQ ID NO:3 and nucleotides 52-783 of SEQ ID NO:3 against all commercial nucleic acid databases including issued patents database and pending application database and provide a print of all results.

SEQ ID NO: 2 and amino acids 40-261 of SEQ ID NO:2 against all commercial protein databases including issued patents database and pending application database and provide a print of all results.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao, Ph.D. Bi technology Patent Examiner Art Unit 1652, Room 10A11 Crystal Mall 1, USPTO.

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Searcher: 18 4lon-10-19
Phone: 308-4501/4506
Location: Brotest lik-
Date Picked Up: 8/15/02
Date Completed: 4/10/02
Searcher Prep/Review:
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TYPE OF SEARCH:	
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DIALOG:
Questel/Orbit:
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Listing first 45 summaries
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1620	61 CGCTTTGTGCCTGACTTTGTAGTGCGCTACGGAGGCGTCAGCCGGCGTGGTGCGTTTCCC	15	
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Johansson,M., Thorbjarnardottir,S.H., Palsdottir,A.,
Hreggyidsson,G.O., Kristjansson,J.K., Holst,O. and Eggertsson,G.
Cloning, sequencing and overexpression of a Rhodothermus marinus
gene encoding a thermostable cellulase of glycosyl hydrolase family
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Submitted (25-SEP-1996) Department of Molecular Biology,
Institution of Biology, Grensasvegur 12, Reykjavik 108,
Location/Qualifiers
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/strain="IT1378"
/db_xref="taxon:29549"
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Streptomyces sp. 11AG8
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Streptomycetaceae; St
                                  2 (bases 1 to 1116)
van Solingen,P., Meijer,D.,
Bolle,R., Power,S.D. and Jor
Direct Submission
                                                                                            Actinomycetales; Streptomycineae; Streptomy 1 (bases 1 to 1116) van Sclingen,P., Meijer,D., van der Kleij,W Bolle,R., Power,S.D. and Jones,B.E. Cloning and expression of an endocellulase Streptomycete isolated from an East African
          Submitted (10-FEB-2000) Microbial International B.V., Archimedesweg
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12A (cell2A) gene
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            cgggcggcagccgcgtggccaccgtggaactggccgggggccacctgggaagtctggtatg 1286
                                                       CCAACGGGGTGAACCGGACCGAGATCATGATCTGGTTCAACCGGGTCGGCCCCGGTCCAGC
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/organism="Streptomyces s/strain="11AG8"
/db_xref="taxon:133452"
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/note="Region: cellulose binding
/132 c 340 g 153 t
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/note="endocellulase"
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1 (bases 1 to 1116)
Jones, B.E., Van Der Kleij, W.A.H., Van Solingen, P. and Weyler,
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                                                     GCAACGGCGTCTACAACGCCGCGTACGACATCTGG-----CTGGACCCGGACACCCCGCA
                                                                                                           TGCCCATGCGGATCAGCTCGATCGGCAGCGCGCCCCAGCAGTGTCTCCTACCGCTACACCG
                                                                                                                                                                AGTCCTATCCCTCGGTCTACGACGGCTGCCACTACGGCAACTGCGCGCCCCCCCACGACGC
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Sequence 2
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Unknown.
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Jones, B.E., Van Der Kleij,W.A.H., Van Solingen,P. and Cellulase producing actinomycetes, cellulase produced method of producing same patent: US 6287899-A 2 11-SEP-2001;
Location/Qualifiers
1. .1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified
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432 c 340 g
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patent US 6287839.
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Pred. No. 5.6e-11;
0; Mismatches 332;
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                                                                                                                                                                                                                                                                                                               cctatccggccatctacttcgggtgccactggggcgcctgcacgagcaattcgggattgc 1049
                                                       gcggcagccgcgtggccaccgtggaactggccgggggccacctgggaagtctggtatgccg 1289
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                                                                                            TCGGTTCGCCGGTCGGCACGGCCCACGTCGGCCGCCAGCTGGGAGGTGTGGACCGGCA
                                                                                                                                              ACGGGGTGAACCGGACCGAGATCATGATCTGGTTCAACCGGGTCGGCCCGGTCCAGCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1716)
Jones, B.E., Van Der Kleij, W.A.H., Van Solingen, P. and Cellulase producing actinomycetes, cellulase produced method of producing same Patent: US 6287839-A 4 11-SEP-2001;
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Sequence 4 from patent US 6287839
AR168362
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1. .1716
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611 c 559 g
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Pred. No. 4.9e-07;
0; Mismatches 227;
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                                      167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-APR-1999) Laboratory of Molecular Genetics, of Biology, Grensasvegur 12, Reykjavík 108, Iceland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1944)
Backman, V., Thorolfsdottir, E.T.T., Kristjansdottir, S.
Thorbjarnardottir, S.H. and Eggertsson, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the groESL, dnaK and dnaJ genes Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; CFB group; Rhodothermus group; Rhodothermus. 1 (bases 1 to 1944)
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AF145250
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                                                    Similarity
                                                                                                                                              385
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submission
                                                                                                                                                                                                                            /product="heat shock protein DnaJ"
/protein_id="AAD37973.1"
/db_xref="G1:5020005"
/translation="MAQAVKDYYEILGVPENATEEEIKKAYRKLAREWHPDRNPDKPN
AEERFKEIQEAYSVLSDPEKRRQYDMMRKNPFGAFGGFGPGNGSRFYRTPEGTYVHFE
                                                                                                                                          RFRREGDDLYTTITINPLEAMLGTTREIVDAYGRRIKVRIPPGTQPGERLRIRGHGVE
TDTHTGDLYVEVQLEIPRNLSAEQQRILREAAEKAGLIRS"
559 c 648 g 352 t
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ALRGGKTDITLPDGQKVRINIPKGVRPGFKIRLKDGGPTIAGVPQGNVYIIFEVEPHP
                                                                                                                                                                                                                                                                                                                                                                           478. .1428
                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="GRRGRSDRTRLGPALDTLEALLDEGAAGTFDLAFIDADKASYDAYYERALQLVRPGGLILLDNLLMGGRVADPSNREPSVEAIRRLNEKLCRDLRVDYALLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative 0-methyltransferase"
/protein_id="AAD37972.1"
/db_xref="GI:5020004"
                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                          LADGLGLARRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rhodothermus
/strain="ITI 376"
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                                  Score 105.2; DB 1
Pred. No. 5.8e-07;
0; Mismatches 48
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U51222.1
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Streptomyces halstedii beta-1,4-endoglucanase (celA2) gene,
complete cds, and cellulose binding protein (p40) gene, com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiologia Bioquimica, Consejo Superior de
Científicas / Universidad de Salamanca, Avda.
s/n, Salamanca, Salamança 37007, Spain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Two genes encoding an endoglucanase and a cellulose-binding protein are clustered and co-regulated by a TTA codon in Streptomyces
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Streptomyces.
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                                                                                                                                                                                                                          /Protein_id="AAC45429.1"
/Protein_id="AAC45429.1"
/db_xref="G1:2209260"
/db_xref="G1:2209260"
/translation="MRALPHGPRTPRSLLGALLLALATVAAVLAAAPAAHADTLVCEQ
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YTNCSPGTNLDAQVSGIASAPSSISYGFVGSAVYNASYDIWLDPTPKKKGVNRTEIMI
YTNCSPGTNLDAQVSGIASAPSSISYGFVGSAVYNASYDIWLDPTPKKKGVNRTEIMI
WLNKVGPIQPIGSQAGTASYGGRTWOVWRGSNGSNDVISFVAPSAVASWSFDVMDFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="celA2"
595. .1728
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                                                                                                                                            TATGLAHSAQVAAGASQTFGFQGTYSGTFSKPSGFSLNGARCA*
                                                                                                                                                                    NT I ARGMAQNNWYLTSVQAGFEPWQNGAGLAVNSFSSTVNLGTPGTGSPGAPGEPVTA
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                                                                                                                                                                                                                                                                                                                                                                                                  /product="Cel2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="beta-1,4-endoglucanase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Streptomyces halstedii"
/strain="JM8"
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                                                     codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="celA2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:1944"
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                                                                             binding protein"
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SOURCE
ORGANISM
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KEYWORDS
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IPPDGSVTFGFTATSTGNNLPVGSIGCVNP"
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Pred. No. 6.9e:
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Best Local Sin
Matches 336;
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TITLE
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                                                                                                                                                                                                                                                                                                                         CCGCGACCGCCCCCGCACAGGCCGACACCACGATCTGCGAAGAGTTCGGCTCGACCGTCA 313
                                                                                                                                                                                                                                                                                                                                                         cgatcacgacgggccgctggaatgccgcctacgacatctggttcagtcccgtcacgaatt 1160
                                    CCGCGCTCCCCGCGCGATCAGCGGCATCTCCTCCGCGCCCAGCAGCATCTCGTACGGCT
                                                         cgggattgccgcggcgcgtgcaggagctgtcccgacgtgcgcacgagctggacgctcacgc 1100
                                                                                                           CGCCGAAGTCGTACCCGTCGGTCTTCAACGGCTGTCACTACACGAACTGTTCGCCGGGCA 493
                                                                                                                               acgtggccgcctatccggccatctacttcgggtgccactggggcgcctgcacgagcaatt 1040
                                                                                                                                                                                 CCGCGACCGACTCCGGCTTCCGGGTCACGCACGCCGACGGCTCGGTGCCGACCAACGGCG
                                                                                                                                                                                                     aggtcggactggaaacgggcaacttcacgatcacgggccgatcacgacaacggcaaca
                                                                                                                                                                                                                                                       TCCAGGGCCGTTACGTCGTCCAGAACAACCGCTGGGGCACCAGCGCCACCCAGTGCGTCA 373
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Gene 148 (1), 119-124 (1994)
95011642
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Direct Submission
Submitted (07-JUL-1993) G. Mastromei, Universita di Firenze, Dipt di Biologia Animale e Genetica, Via Romana, 17/19, 50125 Firenze,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Characterization and sequence
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1321. .1340
1351. .1403
1419. .1453
a 579 c 475 g 205 t
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FGSTVLQGRYVVQNNRRGTSATQCVTATDSGFRVTQAGSSVFUAQFKSYPSVPNGCH
YTNCSPGTALPARISGISSAESISVGFVDNAYVNASYDIWLDDTPRTDOVNRTEINI
WFNRVGQIQPIGSQVGTASVAGRTWEVWSGGNGTNDVLSFVAPSAMSSWSFDVMDFVR
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PAACTVSYATNVWPGGFTANVTVTNNGSAPVDGWRLAFTLPSGQSVVHÄWNASVSPSS
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/db_xref="GI:393392"
/db_xref="SPTREMBL:Q59963"
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/EC_number="3.2.1.4"
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/strain="A2"
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0; Mismatches 372;
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AF130408
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                                                                                                                                                                                                                                                                                                                                                                                                         Characterization and sequence analysis of two genes involved cellulase degradation in Streptomyces viridosporus T7A, and i expression in Escherichia coli
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Bacteria; Firmicutes; Actinobacteria, Actinobacteridae;
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Ramachandran, S. and
                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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/strain="T7A"
/db_xref="taxon:67581"
/product="cellulase"
/protein_id="AAD25090.1"
/db_xref="GI:4583445"
                                                                                                 /note="putative"
157. .1311
                                          /codon_start=1
/transl_table=11
                                                                                  /gene="celS1"
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                                                                                                                                             /rpt_type=inverted
144. .149
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                                                                      note="CelS1;
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                                                 Streptomyces lividans
Streptomyces Streptomyces: Actinobacteria; Actinobacteridae;
Actinomyces Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 1565)
Wittmann,S., Shareck,F., Kluepfel,D. and Morosoli,R.
Purification and characterization of the CelB endoglucanase from Streptomyces lividans 66 and DNA sequence of the encoding gene
Streptomyces lividans 66 and DNA sequence of the Encoding gene
Figure 1 Francisco 1 (5), 1701-1703 (1994)
Direct Sul
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                                                                                                                                                                                                                                Streptomyces lividans U04629
                            Shareck, F.
                                                                                                                                                                                                                  U04629.1
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(bases 1 to 1565)

GI:2462717

66

cellulase

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linear) gene,

complete BCT

02-OCT-1997 ete cds.

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Submission ted (21-DEC-1993)

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Armand Frappier, CRMA,

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CGGTGCGGGGCT 929
                                          cggggccggtct 1461
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ygtttlogryvvqnnrwgsssppcvtardtgfrltqabgsvptwgapksypsverwgch

ytncspgtklparisgissaparisgissapssisygyvggapynasypibldptprt

ytncspgtklparisgissaparisgissapssisygyvwsggngsndvlspvapsaiss

DGVNRTEIMIWENKVEDIQPIGSQVGTATVGGETWQVWSGGNGSNDVLSPVAPSAIES

WSFDVMDFVRETVARGMAQNDWYLTSVQAGFEPWQNGAGLAVNSFSSTVDTGGGTPGG

PGTPAACTVSYATNVWPGGFTANVTVRNTGSSAVDGWRLAFTLPAGQRITQAWNAYRH
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                                                                                                                                                                                                                                        attgccgcggcgcgtgcaggagctgtccgacgtgcgcacgagctggacgctcacgccgat 1104
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                                                                CCTCCCCGTCCGGCTCGACACCGTCTCCGCGGCGCGCCGTCCAGCATCTCGTACGGCTTCGT
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GCCCATCGGCTCACCGGTGGGCACGGCCTCCGTCGGCGGCCGGACCTGGGAGGTGTGGAG
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Sequence update by submitter
On Oct 2, 1997 this sequence version replaced gi:439693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-OCT-1997) Institut Prairies, Laval, Quebec H7N 4Z3,
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EVRATYARGLAENDWYLTSYQAGFEFWQNGAGLAVNSESSTVETGTPGGTDPGDPGGP
SACAYSYGTNYWQDGETADYTYTNTGTAPYDGWQLAFTLPSGQRITNAWNASLTPSSG
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448. .1470
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CEPFGTTTIQGRYVVQNNRWGSTAPQCVTATDTGFRVTQADGSAPTNGAPKSYPSVFN
GCHYTNCSPGTDLPVRLDTVSAAPSSLSYGFVDGAVYNASYDLWLDPTARTDGVNQTE
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/function="hydrolase"
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/clone="IAF12"
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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS. The length in codons is given for each CDS which show significant similarity to other CDS in the database CDS which show significant similarity to other CDS in the database The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (23-NOV-1999) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA E-mail: barrellesanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 70H, UK
                                                                                                                                                                                                                                                                                                   CDS are numbered coelicolor), 787
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betails of S. coelicolor sequencing at the Sanger Centre are
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A set of ordered cosmids and a detailed genetic and physical map
for the 8 mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
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Streptomyces coelicolor A3(2)
Bacteria; FirmLoutes; Actinobacteria; Actinobacteridae;
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Streptomyces coelicolor
AL133210
AL133210.1 GI:6468421
                                                                                                                                                                                                                                                                                              (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.0lc.coelicolor), 7B7 (cosmid name), .0l (first CDS), c (compl
                                                                                                                                                                                                                                                                                                                                                                                   available on the World Wide Web.
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http://www.nih.go.jp/
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d GllA lies on the Asel-G genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Bibb
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                                                                         /gene="SGG11A.02" | Jose repressor, len: 402 aa; /note="SCG11A.02, possible xylose repressor, len: 402 aa; similar to SW:XYLR_BACSU (EMBL:M27248) Bacillus subtilis xylose repressor xylR, 384 aa; fasta scores: opt: 612 z-score: 642.4 E(): 2.1e-28; 29.4% identity in 381 aa overlap. Contains match to Pfam entry pF00480 ROK, ROK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="xylulose kinase"
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/translation="DPROWWDALGEALSQCGGHGLY"
/translation="DPROWWDALGEALSQCGGHGLY"
/translation="DPROWWDALGEALSQCGGHGLY"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="xyl8"
/note="PS00933 FGGY family of carbohydrate kinases signature 1"
874. .936
     family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carbohydrate kinases, 250. .288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="xylB"
/gene="xylB"
/note="Pfam match to entry PF00370 FGGY, FGGY
/note="Pfam match to entry PF00370 FGGY, FGGY
/note="Pfam match to entry PF00370 FGGY, FGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFLDGERTPNLPHSSGLLHGLRHDTTAGQLLQAAYDGAVHSLLGALDLVLDADADPSA PLLLIGGGARGTAWQQTVRRLSGRPVQIPEARELVALGAAAQAAGLLTGEDAAAVARR WNTAAGPVLDAVERDEATLNRITGVLSDAAPLLERDAASR"
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2StG11"
                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SCG11A.02"
1525. .2733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76. .1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="PS00445 FGGY family of carbohydrate kinases
signature 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:100226"
/clone="cosmid F37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="xylB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="xylB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Streptomyces"
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ly and a possible helix-turn-helix motif at residues .64 (+3.15 SD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     et al., Gene 30:157-66(1984) as implemented at
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                                                                                                                                                                                                            gene
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3821. 5080
/gene="SCG11A.04"
3821. 5080
/gene="SCG11A.04"
3821. 5080
/gene="SCG11A.04"
/note="SCG11A.04"
/not
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                                                                                              /gene="thcA"
5218. .6741
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MTDAWLALEPGADPVERARALRRAHETFTEAGTVRRPVRAVVAD
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FIRRVQPWTCAAAPVHDPRTGRVLGAVDITGGDGLAHPHSLGFVQAVARAAESQLALL
TPERSASEAAELTALGRDEALLSADGRRVRLSRRHSEIVVLLAHHPEGLTGDELLCAL
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/brotein_id="GAB61584.1"
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DGHVAQCVRETDIAWHAGNWDYNTRSIGIEHEGWVDRPEYFTNAMYEQSARLTAAICT
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3041. .3646
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/protein_id="CAB61583.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative trans(
/protein_id="CAB61585.1"
/db_xref="GI:6468425"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Pfam match to entry PF01510 Amidase_2,
N-acetylmuramoy1-L-alanine amidase, score 89.80,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYGIPKDRTHIIAHHEVPGSDHTDPGPFWDWTRYIRLVNFA"
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                                                                                                                                                                                                                                                                                                                                                              <u>AAYAGPLLPGSQAPAVGRLRRRLADGLRAALIACGDPDLLADWAHAPWGEDDLDVWRA</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                          LAAVRPTAATSSRLAALESELAAPNPW"
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note="SCG11A.05, thcA, aldehyde dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                              EDETVPPVTLRAELARLRGILGPGRLASRPYRLTMPVESDTSVVERRLRAGAVTAAA
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     1en:534
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VERSION
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Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTGAACTCCTTCTCCTCCACCGTCGAG 28449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gtggtatctgcatgcggtggagacgggcttcgaactctgggagggcggggccggtctgcg 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGCTTCGACGTCATGGACTTCGTCCGGGGGGACCGTCGCGGGGACTCGCCGAGAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      attgccgcggcgcgtgcaggagctgtccgacgtgcgcacgagctggacgctcacgccgat 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGTCGTACCCGTCGGCTTCAACGGCTGCCACTACACGAACTGTTCACCGGGCACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caacggctacagcggcggcgcgagctgatcttggctgaactggaacggcggcgtgat 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGACGGCGCCGTCTACAACGCCTCGTACGACATATGG-----CTGGACCCGACGGCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTCCCCGTCCGGCTCGACACCGTCTCCGCGGCGCGCCGTCCAGCATCTCGTACGGCTTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACCGACACCGGCTTCCGGGTCACGCAGGCCGACGGCTCGGCACCGACCAACGGGGGCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGCGGCAACGGCTCGAACGACGTGCTGTCGTTCGTTGGCACCGTCGGCGATCAGCGGCTG
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                                                 Ng,W.V., Kennedy,S.P., Mahairas,G.G., Berquist,B., Pan,M.,
Shukla,H.D., Lasky,S.R., Baliga,N., Thorsson,V., Sbrogna,J.,
Swartzell,S., Weir,D., Hall,J., Dahl,T.A., Weiti,R., Goo,Y.A.,
Leithauser,B., Keller,K., Cruz,R., Danson,M.J., Hough,D.W.,
Maddocks,D.G., Jablonski,P.E., Krebs,M.P., Angevine,C.M., Dale,H.,
Isenbarger,T.A., Peck,R.F., Pohlschrod,M., Spudich,J.L.,
Jung,K.-H., Alam,M., Freitas,T., Hou,S., Daniels,C.J., Dennis,P.P.
Omer,A.D., Ebhardt,H., Lowe,T.M., Llang,P., Riley,M., Hood,L. and
         Passarma, From the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halobacterium sp. AE005123 AE004437 AE005123.1 GI:10
                                                                                                                                                                                                                                                                                                                                      Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                           Halobacterium sp. NRC-1.
Halobacterium sp. NRC-1
Archaea; Euryarchaeota; Halobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                          (bases 1 to 11202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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         cover:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:1058,1826
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         genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11202 bp
NRC-1 section
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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      sequence
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      of
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4 of
      halobacterium
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                                                                                                                                                                                                                                                                                                                                                                  Halobacteriales;
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      species
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PUBMED
REFERENCE
AUTHORS
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JOURNAL
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2 (bases 1 to 11202)
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                                                                                                                                                                                                                                                                                                                                   /gene="glcD"
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2715. .5753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAG20507.1"
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/protein_id="AAG20508...
/db_xref="GI:10581828"
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1351. .2646
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/note="GlcD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLDSGYGGMLTFGVEDGYEAAQSVTEETTLASLLANVGDAKTLVIHPASTTHQQLTPE
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/transl_table=11
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76. .1281
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Submitted (12-JAN-2001) RRAT, Centers for Disease Prevention, 1600 Clifton Road, Atlanta, GA 30333, Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burkholderia pseudomallei Bacteria; Proteobacteria; beta subdivision; Burkholderia Burkholderia; pseudomallei group.
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                                                                                                     AGCCGGCGAGCGCCGCCGTCAGCGCGACGAGCGCCGCGACGGCGGCACCGTCATCCCGA 1763
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                                                                                                                                                      CGAGCTTGGCCTCGCGCGGCCGGCCGAGGAACACGATGCCGAAGAACTTGACCATCGCGT
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                                                                                                                                                                                                                                                                                                      Score
             131.8
131.8
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AAV72359 standard; DNA;

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AAV72359;

28-JUL-1999

(first entry)

Actinomycete sp. 36kD cellulase DNA

24-JUN-1998; 19-NOV-1997; 19-NOV-1997; Cellulase; detergent; animal feed; nutritional value; textile; stone washing; texture modification; appearance; cellulosic fabric; pulp; draining; paper; baking additive; starch treatment; grain; high:fructose corn syrup production; ethanol production; fibre reduction; W09925846-A2 27-MAY-1999. Actinomyces sp. (GEMV) GENENCOR INT INC 18-NOV-1998; BE, Van 98US-0104308. 97US-0974041. 97US-0974042. Der Kleij WAH, 98WO-US24649 Van Sollingen ۵, Weyler Σ

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P-PSDB; AAY08473.
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18-NOV-1998;
28-MAY-1999;
                                                                                                                                                                                     The invention provides a cellulase from Actinomycetes. The cellula be used in a detergent composition, as an additive for animal feed for the treatment of textiles or pulp and paper. The DNA encoding cellulase can be used to identify homologous cellulases and for recombinant production of cellulases. The present sequence represe
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DB; AAY67496.
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98US-0104308
                      99WO-US11971
                                                                                                           /*tag= c
/note= "mature:
1576..1715
                                                                                                                                            /*tag= b
/note= "CelA signal sequence"
549..1564
                                                                                                                                                                              /*tag= a
/note= "GI promoter
407..548
                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      DNA; 1715
                                                                                      "11AG3 downstream sequence containing
                                                                                                                        11AG8
                                                                                                                                                                                          sequence"
                                                                                                                       sequence'
                                                                                                                                                                                                                                                                                              feed additive;
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Best Local S
Matches 345
 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides a cellulase from Actinomycetes. The cellulase to be used in a detergent composition, as an additive for animal feed and for the treatment of textiles or pulp and paper. The DNA encoding the cellulase can be used to identify homologous cellulases and for recombinant production of cellulases. The present sequence represents the DNA sequence of a complete expression cassette consisting of the opposition of cellulases.
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P-PSDB; AAY67497.
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28-MAY-1999;
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                                                                   99cagccgcgtggccaccgtggaactggccggggccacctgggaagtctggtatgccgac 1291
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99US-0321981.
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Best Local Similarity 51.0
Matches 213; Conservative
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                                                                                                                                                                                                                                                  Transgenic plants such as Cichorium intybus, Cynara scolymus, Helianthus tuberosus, Scorzonera hispanica, Oryza sativa, Zea mays, Triticum aestivum, Triticum durum, Hordeum vulgare, Secale cereale, Avna sativa, Sorghum vulgare, Phleum pratense, Lolium temulentum,
                                                                                                                                                                                             Dactylis glomerata, Pennisetum americanum, Allium cepa, Agave americanum, Agava azul teqilana, Sorghum bicolor and Panicum mile transformed with a vector encoding a fructan exohydrolase (FEH) enzyme are useful for the recombinant production of FEH or other polypeptides having FEH activity. The FEH polypeptides produced are useful in detergents or as a detergent additive and in oral
                                                                                                                                                                    Sequence 1983 BP;
                                                                                                                                                                                                                                                                                                                     compositions, and in detergents
                                                                                                                                                                                                                                                                                                                              Novel DNA molecules encoding enzymes activity for use in transgenic plant
                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-007401/01.
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                 aacgtggccgcctatccggccatctacttcgggtgccactggggcgcctgcacgagcaat
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                                                                               gccggggtgcggcacgtgctgaagctcagcgtgatggacacgctccaggaccactacatg
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             /note= "fkbJ gene"
complement (11244..12092)
                                                                                                /note- "fkbG gene"
complement (9122..9883)
                                                                                                                                                                                                               /note= "fkbR2 gene"
complement (4595..5488)
                                          /note- "fkbI gene" complement (10987..11247)
                                                                                                                               8156..8824
                                                                                                                                                            6808..8052
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                                                                                                                                                                                                                                                                      complement (2020..3579)
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     /*tag=
                                                                     complement (9894..10994)
                                                                                 /note- "fkbH gene"
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/note= "fkbV gene"
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                                                                                                                                      gacgggaagcagctgcggcagtggccggtggaggagatagaaacgctgcggaggaagcgc
                                                                                                                                                                                                                                                                        gccgacgacgtcgccaagggctggtccggcacgttcccgcggaagctgtggctggacgag 1092
                                                                                                                                                                                                                                                                                                                                                                                                                      ttcgacgcgcgggagccggcgtgctgtgggcgtgggccaacgagtccgacagccag
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Streptomyces hygroscópicus var. ascomyceticus; immunophilin; FK-506 binding protein; polyketide compound; transplant rejectio graft-versus-host disease; uvatitis; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; multiple sclerosis; primary biliary cirrhosis; scleroderma; neurite outgrowth; nerve regrowth; parkinson's disease; Alzheimer's disease; stroke; traumatic spinal cord; brain injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA14651 standard; DNA; 77536
                                                                                                                                                                                                                                                                                                                   FK-520; polyketide synthase; PKS; gene cluster;
                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of the FK-520 biosynthetic gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
             brain injury;
                                                                                                                                                                                                                                 rejection;
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misc_feature misc_feature misc_feature	misc_feature	misc_feature	misc_feature misc_feature	misc_feature	CDS misc_feature	misc_feature	,	misc_feature misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	CDS
	<pre>/note= "KR3" complement (2986931018) /*tag= af /note= "DH3 (inactive)" complement (3101832185) /*tag= ag</pre>	/note= "K94" (2875028960) (complement (2875028960) /*tag= ad (note= "ACP3" (complement (2909229740) /*tag= ae	complement (2614627430) /*tag= ab /note= "AT4" complement (2743028684) /*tag= ac	/*tag= z /note= "ACP4" complement (2499726146) /*tag= aa /note= "DH4 (inactive)"	complement (2399246573) /*tag" y /note= "fkbB gene" complement (2416324373)	/note= "AT5" complement (2265323892) /*tag= x /note= "KS5"	(21420	<pre>complement (1946420097) /*tag= u /note= "KR5" complement (2024121420)</pre>	/note= "KS6" complement (1911619326) /*tag= t /note= "ACP5"	/*tag= r /note= "acyltransferase domain (AT) 6" complement (1782019053) /*tag= s	a .	/*cag* p /note= "ER6" complement (1543816587)	/*tag= 0 /note= "KR6" complement (1451715294)	/*tag= n /note= "ACP6" complement (1376114394)	/*tag= m /note= "fkbC gene" complement (1345213662)	complement (1211313150) /*tag" 1 /note= "fkbL gene" complement (1321223988)
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RESULT
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Best Local Similarity 48.4%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000
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/note= "ORF 27;
5806..12294
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/note= "ORF 29;
2767..3486
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/transl_except=
/note= "ORF 30;
561..2309
               /*tag=
/note=
21010..
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/note= *ORF 28;
3527..5593
                                                            /note-
15488..
                                                                                          /*tag=
                                                                                                         12291
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/note= "ORF 26;
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                        ..1549
                                                            .21013
                     g
"ORF 24; encodes AAB07562
                                                                       "ORF 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53.6; DB 21;
Pred. No. 0.032;
0; Mismatches 159;
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                                                                                                                                                                  (pos: 1..3, aa: Met) encodes AAB07559"
                                                                                                                                                                                                                                                                       (pos: 1..3, aa: Met)
encodes AAB07557"
                                                                                                                                                                                                                             encodes AAB07558"
                                                                         encodes
                                                                                                                        encodes
                                                                          AAB07561"
                                                                                                                      AAB07560'
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 CONTRACTOR OF THE PROPERTY OF 
WPI; 2000-465974/40.
P-PSDB; AAB07556, AAB07557, AAB07558, AAB07559, AAB07560, AAB07561, AAB07562, AAB07563, AAB07564, AAB07565, AAB07566, AAB07567, AAB07568
                                                            Shen
                                                                                                                    06-JAN-1999; 99US-0115435
05-FEB-1999; 99US-0118848
05-JAN-2000; 2000US-0477962
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/transl_except=
/note= "ORF 15;
50998..52386
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/note= "ORF 18;
39301..47181
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/note= "ORF 9; 6
57583..58857
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/note= "ORF 12;
54187..55824
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53018.
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/note= "ORF 20;
35818..37302
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/note= "ORF 10;
56090..57586
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55821..56093
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/note= "ORF 16;
49982..51001
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47178..
                                                            Sanchez
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/note= "ORF 19;
37299..39215
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/note= "ORF 23;
24663..32690
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/transl_except=
/note= "ORF 14;
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32893..34830
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                                                            Chen
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encodes AAB07577"
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                                                            Edwards
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AAB07576"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the BLM (Bleomycin) gene cluster, containing open reading frames (ORFS) 8-30. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically modifying biological molecules to produce branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an apo-carrier protein and coenzyme A to produce a holo-carrier protein. The BLM gene cluster or catalytic domains can be used individually or collectively to produce thiazolidine, thiazoline, bithiazoline and bithiazoline-containing microbial metabolites. The BLM gene cluster may also be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 58857 BP; 7256 A; 25139 C; 19353 G; 7109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 97-136; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New bleomycin gene cluster components useful for peptide and/or polyketide metabolites, especially bleomycin, production and for chemically modifying biological molecules -
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                                                                   collagen;
                                                                                                     Collagen-like polymer sequence D gene 2 encoding unit C2A24C2
                                                                                                                                                                                                              AAT16766 standard;
                                                  photographic;
                                                                                                                                            24-FEB-1997
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                                                                                                                                                                                                                                                                                                      accgcgtcgacgtcacggccaccctcccggacggcgcccccga
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                                                                   repetitive triad motif; recombinant production;
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                                                    medical; structural;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention concerns collagen-like polymers having repetitive triads with reduced proline content, and where glycine is the initial amino acids and the subsequent amino acids are varied. The choice of triads utilised in a recombinant collagen-like polymer are chosen in order to affect properties such as helix stability, hydration, solubility, gel point, biodegradation and immunogenicity. Triads of particular interest include GAP, GPA, GPP, GAS, GPG, GPS, GAQ, GSP, GIQ, GPR, GPK, GAR, GER, GDR, GEP, GDA, GAH and GEA. The collagen-like polymers may impart compared to the collagen of being produced in unicellular microorganisms at high mol. wts. and in high efficiency. Plasmid DNA from several colonies were analysed for inserts contg. Complished BNA fragments by digestion with Fokl. The present sequence, was identified to contain the SequenceD gene 1 monomer sequence C2A24C2. The SequenceD collagen-like polymers are used as immunogens for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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06-NOV-1990;
12-NOV-1991;
                   1192
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gatgatctggctgaactggaacggcggcgtgatgccgggcggcagccgcgtggccaccgt 1251
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                                                                         cgacatctggttcagtcccgtcacgaattccggcaacggctacagcggcggcggcgagct
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                                                                                                                                                                                                                                                                                                              cacacgggccgatcacgacaacggcaacaacgtggccgcctatccggccatctacttcgg 1011
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90US-0609716.
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                                                                                      Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                             The present sequence is a putative coding sequence for the wheat 1-deoxy-D-xylulose 5-phosphate synthase enzyme (DXPS). Its protein is involved in the isoprenoid biosynthesis pathway. The cDNA was identified by sequencing a number of clones and then comparing their protein sequences to known proteins: this showed the sequence's similarity to the Capsicum annuum DXPS sequence. The DXPS gene and protein can be used to create transgent plants which express the gene at either different levels or at different stages of development compared to normal, and to identify herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide encoding 1-deoxy-D-xylulose 5-phosphate synthase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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The sequences given in AAO43030-34 encode examples of recombinantly produced DCP collagen-like polymers (CLPs) which consist of repeated tripeptide sequences selected from a wide range of GXY sequences, where X and Y can be any amino acid. These sequences can be cloned into plasmids and used to transform E. coll to produce the DCP proteins. DCP peptides comprise repeated units of; A = GARGPAGPP, B = GSRGDPGPP and/or C = GAHGPAGPK. These polymers may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1118
                                                                                                                               High mol. wt. collagen-like protein polymers -
produced in unicellular microorganisms
                                                                                                                                                                                                          Cappello
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                                                                                                                                                                                    WPI; 1993-182496/22.
                                                                                                                                                                                                                                                                                       04-NOV-1992;
                                                                                                                                                                                                                                                                                                                 27-MAY-1993
                                                                                                                                                                                                                                                                                                                                          WO9310154-A
                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Collagen-like polymer DCP3-C2(AB12)C2 coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ43032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ43032 standard;
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                                                                                                                                                                      P-PSDB; AAR37738.
                                                                                                                                                                                                                                    (PROT-) PROTEIN POLYMER TECHNOLOGIES
                                                                                                                                                                                                                                                               12-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                           hydrogel;
                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant; collagen-like polymer; CLP; tripeptide; helix;
                                                                                                                                                                                                                                                                                                                                                                                                       ibre;
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interchain
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                                                                                                                                                                                                                                                                                                                                                                                           linkage;
                                                                                                                                                                                                                                                                                                                                                                                           triad sequence;
linkage; colloid
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                                                                                                      English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        raise anti-DCP antibodies in rabbits. These polymers have molecular weights of >30 kD and are able to form helices due to interchain linkages. These polymers pref. contain a proportion of tripeptide triad sequences found in natural collagens, pref. mammalian collagens. The CLPs impart unique characteristics to materials such as fibres, membranes, films, coatings, hydrogels, colloid suspensions and moulded
               07-OCT-1997;
                                                                                                 Mycobacterium
                                                                                                                                            Tuberculosis;
                                                                                                                                                                                                                                                           AAV64548
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les 223; Conserv
                                                                                                                                                                     tuberculosis immunogenic polypeptide XP25 3'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atggggcgcggagaccgcccagtgcattgaggtcggactggaaacgggcaacttcacgat 951
                                                                                                                                                                                                                                                                                                                                               ctaccggcgcacgacgcccaccacgtcggtgag 1344
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                                                                                                                                                                                                                                                                                                                                  cgccaggtgcccatggcccagcaggaccgaaag
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                                                                                                                           pharmaceutical;
                                                                                                                                                                                                                                                           standard;
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                                                                                                                                                                                                   (first
                                                                                                                                          immunogenic;
                                                                                                 tuberculosis
               97WO-US18293
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                                                                                                                                                                                                  entry)
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                                                                                                                           :; soluble;
infection;
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Pred. No.
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                                                                                                                           antigen; p
diagnosis;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis (MT) antigen which can be used in a method for i protective immunity against tuberculosis (TB). This sequence formulated into vaccines and/or pharmaceutical compositions f immunising against M. tuberculosis infection or may be used fingnosis of tuberculosis.
                                                  1309
                                                                                                                                                                                                                                                        1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 176; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campos-Neto A, Dillo
Reed SG, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - uso to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-1997;
11-OCT-1996;
  714
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                                  ctacgacatctggttcagtcacgaattccggcaacggctacagcggcggcgcga
                                                                                                                                                                                                                                                                                                                                                                                                                                      gtccgacgtgcgcagctggacgctcacgccgatcacgacgggccgctggaatgccgc
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cacctgatcggcctagccgcacccgggaaagccgatccaacaggcgacgatgcc
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Best Local
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                                                                                                                                                                                                                                                                                                                              extrapulmonary tuberculosis. It bears no similarity to known sequences. The invention relates to methods and compositions for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of a M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the 3' region of DNA coding for an antigenic portion of Mycobacterium tuberculosis antigen xP25; 5' DNA is provided in AAV44438. XP25 DNA was isolated from a M. tuberculosis strain Erdman genomic DNA expression library using sera from patients having extrapulmonary tuberculosis. It bears no similarity to known
                                                                                                                                                                                                                                                                                        Sequence 985 BP; 138 A; 330 C; 423
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Reed SG, Skeiky YAW,
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11-OCT-1996;
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                                                                                                                                                                                tttcccgatggcgacaacggaaaggaaccggagcctgagcccgagccgaccgtcgagctg
acacgggccgatcacgacaacggcaacaacgtggccgcctatccggccatctacttcggg
                                                    gccggcggccgcggtgacggcgatggggccagcggtctcggcctgggcctctcc
                                                                               tggggcgcggagaccgcccagtgcattgaggtcggactggaaacgggcaacttcacgatc
                                                                                                           acc99tacc99c9gcacc99c9gc9tt9tc99cgccacc99tagtgcaggcatc9gc9g9
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                                                                                                                                                               4; Page 187-188;
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Vedvick TS;
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        The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects, AAZ19249 to AAZ19460 and AAY39083 to
                                                                                                                                                         Claim
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                                                                                                                                                                                   New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                    05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis; M. tuberculosis; immunotherapy; diagnosis; immunisation; vacci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. tuberculosis antigen 3'
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YAW, Twardzik |
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R, Vedvick
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Best Local Similarity 44.9
Matches 267; Conservative
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               05-MAY-1998;
18-FEB-1998;
                                                                                26-AUG-1999
                                                                                                       W09942118-A2
                                                                                                                                 Mycobacterium
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                                                                                                                                                                                                                                                       AAZ19137;
                                                                                                                                                                                                                                                                               AAZ19137 standard;
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                                                     17-FEB-1999;
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                                                                                                                                   tuberculosis
               98US-0072596.
98US-0024753.
                                                     99WO-US03265
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                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                       detection; infection; antibody;
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RESULT 14
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ID AAS086
XX
AC AAS086
XX

standard;

DNA;

12152 BP

AAS08699 AAS08699

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Best Local Similarity
Matches 267; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                             1069
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714 cacctgatcggcctagccgcacccgggaaagccgatccaacaggcgacgatgcc
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                                                                                                                                                                                                                                             gccgcaggtctcggcgacaacggcggggtcggcggtgacggtgggggc-cggtggcgccgc
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Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217; 323pp;
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Pred. No. 0.16;
0; Mismatches 322;
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R, Vedvick TS;
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P-PSDB; AAU04901, AAU04902, AAU04903, AAU04904, AAU04905, AAU04906, AAU04907, AAU04908, AAU04909, AAU04910, AAU04911.
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New nucleic acid molecules encoding everninomicin pathway gene
                             WPI; 2001-442147/47
                                                          (SCHE
                                                                        12-JAN-2000; 2000US-0175751
                                                                                       12-JAN-2001; 2001WO-US01187
                                                                                                       19-JUL-2001.
                                                                                                                                                                                                                                        RBS
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                                            Hosted
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                                                                                                                                                                RBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Everninomicin; antibiotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  termentation;
                                                           ) SCHERING CORP
                                            TJ,
                                            Horan AC, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                               /*tag= o
/product= "
9568..9571
                                                                                                                                 /product=
                                                                                                                                                                                                                                                            complement (7280..8133)
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complement (4280..4284)
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                                                                                                                                                                                                                                      complement (8141..8145)
                                                                                                                                                                                                                                                                                               complement (6152..6156)
                                                                                                                                                                                                                                                                                                                                                                              complement (3766..4276)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                    "ORF11"
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                                                                                                                                                                                                           "ORF9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "ORF1"
                                                                                                                                                                                                                                                                                                        "ORF6"
                                                                                                                                                                                                                                                                                                                                                                                                             "ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bottle-neck gene; orthomicin;
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Query Match Best Local S Matches 166

Similarity

45.98;

166;

Conservative

0;

Score 48.4; Depred. No. 0.32 O; Mismatches

DB . 32; 196; 22;

Indels Length 12152;

0;

Gaps

0

Sequence 12152 BP; 1675 A; 4502 C; 4475 G; 1500 T; 0 other;

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everninomicin analogues/homologues and drug discovery. The DNA encoding the integrase allows for increasing a given gene dosage. The integrative vector can be used to permanently integrate copies of a heterologous gene of choice into chromosomes of different hosts and to integrate genes which increase the yield of known products or to generate
                                                                                                                                                                                                                                                                                                                                                                                                                          modified orsellinic acid groups contained in everninomicin, for expressing functional or mutant everninomicin biosynthetic enzyme for evaluation, diagnosis and preferably biosynthesis of everninomicin or other secondary metabolic products, improving the yield of everninomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is useful for selecting for a transfected or transformed host cell. An integrative version of the vector is useful for introducing a everninomicin pathway gene (a bottle-neck gene) into an actinomycete of the genus Micromonospora. The DNA encoding the biosynthetic proteins is useful for synthesising novel everninomicin-related compounds, arising from modifications of the DNA sequence designed to change glycosyl and
                                                                          novel products such as hybrid antibiotics or other novel secondary metabolites. The vector can also be used to integrate antibiotic resistance genes in order to carry out bioconversions with compounds to which the strain is normally sensitive and is thus useful in fermentation
                                                                                                                                                                                                                                                                                                                                and to produce novel everninomicins and also as a hybridisation probe identify homologous sequences. The encoded polypeptides are useful for combinatorial biosynthesis to generate libraries of orthomycins, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 products, useful for improving yields of everninomicin, to produce everninomicin and as probes to identify homologous sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence encodes 11 proteins comprising enzymes of everninomicin antibiotic biosynthetic pathway. A vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erninomicin antibiotic biosynthetic pathway. A vector comp
carbonacea everninomicin biosynthetic pathway resistance
                                                  involving
                                                  e.g. Streptomyces antibioticus
                                                                                                                                                                                                                                                                                                                                                                                                                       improving the yield of everninomicins
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                            AAI99683 standard; DNA; 4403765
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AAI99683;
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Db 3963722 GTCGGGTTCGGGAATACCGGCAACAACAACGTCGGCACCGGAAACGCCGGCAGCGGCAAC 3963663
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Best Local Similarity
Matches 208; Conserv
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                                                                                                                                           3963602 ATCGGTTTCGGCAACACCGGCAACGGCAACATCGGCTTCGGGCTCACCGGCAACAACCAG 3963543
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3963542 GTGGGCATCGGTGGGCTGAACTCGGGCAGCGGAAACATCGGCTTGTTCAACTCGGGCACC 3963483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37RV (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                      1097 acgccgatcacgacgggccgctggaatgccgcctacgacatctggttcagtcccgtcacg 1156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO
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GCGAATGTGGGCATCGGAAACTCGGGGGCCACCGTGGGCCCGTTCGTGGCGGGCCATAAC 3963363
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Search completed: August 19, Job time: 13327 sec 2002, 13:37:08

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1277 gtctggtatgccgactgggactggaattacatcgcc 1312

ACCGGTTTCGGGAACTCGGGTTCGCTCAACACGGGC

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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131.8
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1877
1 gggcgagtcgaacgtcgggc.....tctccgacacttacaaacac 1877
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Gapop 10.0 , Gapext 1.0
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    GenCore version 4.5
Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
                                     Length
  1 US-08-125-468-1

2 US-08-474-933-1

2 US-08-273-508-1

2 US-08-265-310-1

3 US-08-255-310-1

4 US-08-40-856A-9

2 US-08-804-227C-7

9 US-08-804-227C-7

9 US-08-804-108-1

1 US-09-156-856-203

1 US-09-156-856-203

1 US-09-105-537-3

1 US-09-105-537-3

1 US-09-105-537-5

1 US-09-105-537-5

1 US-09-105-537-5

1 US-09-105-537-5

1 US-09-320-878-19

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1 US-09-325-691-4

1 US-09-343-428-1

1 US-09-478-816-1
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4 US-09-321-981-2

4 US-09-321-981-6

1 US-08-642-255-50

4 US-09-056-556-182

4 US-09-103-840A-2
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Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 50, Appli
Sequence 182, App
Sequence 1, Appli
Sequence 2, Appli
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Sequence 203, Appli
Sequence 203, Appli
Sequence 203, Appli
Sequence 5, Appli
Sequence 5, Appli
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Sequence 1, Appli
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Query Match
Best Local Similarity
Matches 347; Conserv

Conservative

7.0%; 50.7%;

Score 131.8; Pred. No. 1.7e 0; Mismatches

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Length 1116;

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	1500 1273 1333 599 20235 20235 20235 1158 71989 432 1155 633 2563 2563 2563 18994 411529
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ALIGNMENTS	US-09-593-711A-10 US-09-319-892-3 US-09-372-422A-9 US-09-372-422A-3 US-07-642-734C-3 US-08-439-009A-3 US-09-443-501A-2 US-09-443-501A-2 US-08-387-942C-7 US-08-387-942C-7 US-08-912-264-2 US-08-912-182-5 US-08-912-182-5 US-08-912-182-5 US-08-912-182-5 US-08-919-953-5
	Sequence 10, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 21, Appli Sequence 21, Appli Sequence 48, Appli Sequence 7, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli

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COMPUTER: LDW COMPUTER: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/104,308
FILING DATE: 24-JUN-1998
PRIOR APPLICATION NUMBER: 08/974,042
APPLICATION NUMBER: 08/974,042
FILING DATE: 19-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC339
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7555
TELEPHONE: 650-846-7555
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US-09-104-308-2
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GENERAL INFORMATION:
GENERAL INFORMATION:
Jones, Brian E.
APPLICANT: Jones, Brian E.
APPLICANT: Van Der Kleij, Wilhelmus A.H.
APPLICANT: Van Solingen, Piet
APPLICANT: Weyler, Walter
TITLE OF INVENTION:
No. 6187577el Cellulase Producing Actinomycetes,
TITLE OF INVENTION:
Cellulase Produced Therefrom and Method of Producing
                                                                                                   TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc
STREET: 925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 925 Page 1
CITY: Palo Alto
STATE: California
                     TYPE: nucleic acid
STRANDEDNESS: single
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TOPOLOGY:
                                                                           LENGTH: 1116 base pairs
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US-09-321-981-2
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                                                                           CURRENT APPLICATION NUMBER: US/09/321,981
CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: PCT/US99/11971
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 09/104,308
PRIOR TILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 09/974,042
PRIOR APPLICATION NUMBER: 08/974,042
PRIOR APPLICATION NUMBER: 1997-11-19
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                        PRIOR FILING DATE: 199
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 2
LENGTH: 1116
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                     APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: No. 6287839el Cellulase Producing Actinomycetes,
TITLE OF INVENTION: Cellulase Produced Therefrom and Method of Producing
                                                                                                                                                                                                 FILE REFERENCE:
ORGANISM: Unknown
              TYPE: DNA
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                                                                                                                                    APPLICANT: Genencor
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: GC54
                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                     Sequence 4, Application US/09321981 Patent No. 6287839
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CURRENT APPLICATION NUMBER: US/09/321,981 CURRENT FILING DATE: 1999-05-28 PRIOR APPLICATION NUMBER: PCT/US99/11971 PRIOR ETLING DATE: 1999-05-28 PRIOR APPLICATION NUMBER: 09/104,308 PRIOR FILING DATE: 1998-06-24
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Local Similarity 50.7%;
nes 347; Conservative
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Cellulase Produced Therefrom
                                                                                                                                                                                International, Inc.
No. 6287839el Cellulase Producing Actinomycetes,
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Pred. No. 1.7e-21;
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    Streptomycetes

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SEQ ID NO 4
LENGTH: 1716
                                                                                                                                                                                                                                               Sequence 50, Application US/08642255 Patent No. 5773249
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 269; Conservative
                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: CAPPELLO, Joseph

APPLICANT: FERRARI, Franco A.

TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Unknown
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                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM
                        STREET: 4 Embarcaderc
CITY: San Francisco
STATE: California
COUNTRY: USA
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                  94111-4187
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                                                                                   E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
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Pred. No. 1.6e-15;
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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic"
US-08-642-255-50
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Best Local Similarity
Matches 223; Conserv
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REFERENCE/DOCKET NUMBER: A5556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEPAX: (415) 494-8771
TELEX: 910 277299 FHT UR
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 50:
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LENGTH: 756 base pairs
TYPE: nucleic acid
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ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I
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COMPUTER: II
                   ctaccggcgcacgacgcccaccacgtcggtgag 1344
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CGCCAGGTGCCCATGGCCCAGCAGGACCGAAAG
                                                                        CAGGCCCGCCAGGTGCGCCTGGACCGGCTGGTCCACCGGGTGCTCCGGGGACCTGCAGGCC
                                                                                                                                                 GACCTGCAGGCCCAGGTGCGCCTGGACCGGCTGGTCCACCGGGTGCTCCGGGACCTG
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 Mismatches

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US-09-056-556-182 ; Sequence 182, Application ; Patent No. 6350456

US/09056556

GENERAL INFORMATION:

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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 985 base pairs
TYPE: nucleic acid
STRANDENNESS: 4141
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                                   1189
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NAME: Mak1, David J.
REGISTRATION UNMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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Local Similarity 44.9%;
les 267; Conservative
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                    gctgatgatctggctgaactggaacggcggcgtgatgccgggcggcagccgcgtggccac 1248
                                                                                        ctacgacatctggttcagtcacgaattccggcaacggctacagcggcggcggcga 1188
                                                                                                                                                                    gtccgacgtgcgcacgagctggacgctcacgccgatcacgacgggccgctggaatgccgc 1128
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                                                                                                                                                                                                                                                                                                             acacgggccgatcacgacaacggcgacaacgtggccgctatccggccatctacttcggg 1012
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GGGCAATGGCGGCAACGGGGGCGCCGGCGGCGGTGCTGGCGGGGGCCGGCGACAACAATTTCAA
                                                                   CGGCAACGGCGCAACGCGGGGGGGTCGGCCTGACAGCCCAAGGCCGGCGACGGCGGCGCGC
                                                                                                                                           GCCGCAGGTCTCGGCGACAACGGCGGGGGTCGGCGGTGACGGTGGGGGC-CGGTGGCGCCGC
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Pred. No. 0.014;
0; Mismatches 322; Indels
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APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, OWEN R.
APPLICANT: WHITE, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 2
SOFTWARE: PATENTIN VET: 2.1
TYPE: DNA
TYPE: DNA
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US-09-103-840A-2/c
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             3963662
                                                                                                                                                                                  3963482 AACAACGTCGGTTTCTTCAACTCCGGCAACGGCAACCTGGGTATCGGCAACTCCAGCGAC
                                                                                                                                                                                                                                                                                                                                                                     3963602 ATCGGTTTCGGCAACACCGGCAACGGCAACATCGGCTTCGGGCTCACCGGCAACAACCAG 3963543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3963722 GTCGGGTTCGGGAATACCGGCAACAACATCGTCGGCACCGGAAACGCCGGCAGCGGCAAC
3963362 ACCGGTTTCGGGAACTCGGGTTCGCTCAACACGGGC 3963327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                          1157 aattccggcaacggctacagcggcggcggcgagctgatctggtctggactggaactggaacggc 1216
                                                                                                                                                                                                                                                                                                     1040 tcgggattgccgcgtgcgcgtgcagg---agctgtccgacgtgcgcacgagctggacgctc 1096
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                                 gtctggtatgccgactgggactggaattacatcgcc
                                                                                                                ggcgtgatgccggggcagccgcgtggccaccgtggaactggccgggggccacctgggaa 1276
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                                                                                          GCGAATGTGGGCATCGGAAACTCGGGGGCCACCGTGGGCCCGTTCGTGGCGGGCCATAAC 3963363
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45.6%;
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Pred. No. 0.13;
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Best Local Similarity
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NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 13241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Ryan,
                                                                                                                                                        24842
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INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Strathy, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlortetracycline and tetracyline Formation and cosmids
TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             1084
                                                                                                                                                                                                                                                                           1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,468
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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CITY: Wayne
STATE: New J
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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ZIP: 07470
                                                                                                   cagtcccgtcacgaattccggcaacggctacagcggcggcgccgagctgatctggct 1203
                                                                                                                                                                               gagctggacgctcacgccgatcacgacgggccgctggaatgccgcctacgacatctggtt 1143
                                                                                                                                                                                                                                                        cgcctgcacgagcaattcgggattgccgcgggggggtgcagggggctgtccgacgtgcgcac 1083
                                  gaactggaacggcggcgtgatgccgggcggcagccgcgtggccaccgtggaactggccgg 1263
                                                                                                                                                    GGTC---GCGCTCGACCGCAGCCGGATGAACCCCGGAGGACGTCGGCTACGTCAACGCGCA 24786
                                                                                                                                                                                                                                  CAACTCCTACAGCATGACCGGGCTGCGGGGTCGACGGGAACGAGGATGGCCGAGGCTATCCG 24843
                                                                                                                                                                                                                                                                                                             GCACGCGATCCGGCGCGCGCGCACATCTACGCCGAGGTCACCGGCTACGCCGGGCGCTG
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GGGCGACCACGCCTACCGGGTGCCGGTCAGCTCGATCAAGTCGATGATCGGACACTCGCT 24669
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45.3%;
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; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-474-933-1
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                                                       Query Match 2.5%;
Best Local Similarity 45.3%;
Matches 253; Conservative
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                                                                                                                                                                                                                                                                                         TELEFAX: (201)831-330:
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pai
                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (201)831-3241
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Cloning of the biosynthetic pathway for TITLE OF INVENTION: chlortetracycline and tetracyline Formation and cosmids TITLE OF INVENTION: useful therein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lotvin, Jason A.
904 gaccgcccagtgcattgaggtcggactggaaacgggccaacttcacgatcacacgggccga 963
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                                                                                                                                                                                                                 LENGTH: 30001 base pairs TYPE: nucleic acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                            NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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Fantini, Susan E.
                                                                                                                                                                                                                                                                                                                    (201)831-3305
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                                                       Score 47.6; DB 2;
Pred. No. 0.056;
0; Mismatches 299;
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                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                 APPLICATION NUMBER: US/00
FILING DATE: 23-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
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        ELECOMMUNICATION
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                                                                                                                                                                                                                          COUNTRY: W
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/125/CACO
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     ADDRESSEE:
STREET: 3(
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Jenish, David
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Best Local Similarity
Matches 185; Conserv
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME/KEY:
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LOCATION: 146..148
OTHER INFORMATION: /note= "Met
OTHER INFORMATION: represents
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                                                           Butler, Michael J.
Hadary, Dany
Jenish, David
Krieger, Timothy
    Krygsman,
                   Walczyk, Eva
                                  Soostmeyer, Gisela
                                               Malek, Lawrence T
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME/KEY:
LOCATION:
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REFERENCE/DOCKET NUMBER: 187
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEPAX: 202 672 575
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APPLICATION NUMBER: US 08/173,508
FILING DATE: 23-DEC-1993
ATTORNEY/ACENT INFORMATION:
NAME: BENT, Stephen A
REGISTRATION NUMBER: 29,768
                    1260 ccggggccacctgggaagtctggtatgccgactgggactgg---aattacatcgcctacc 1316
                                                                                                          1200
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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339 CGGGCATCGACTGGGAGGACTGCGCAGCCGACTGGAACCTGCCCAAGCCCATCCAGTGCG
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LOCATION: 146..148
OTHER INFORMATION: /note= "Met at position -39
OTHER INFORMATION: represents fmet"
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                        Local Similarity
nes 185; Conserv
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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VENTION: STREPTOMYCES
VENTION: STREPTOMYCES
VENTION: POLYPEPTIDES
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LENGTH: 1908 base pairs
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TELECOMMUNICATION INFORMATION:
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NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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 NAME/KEY:
                                                OTHER INFORMATION: /product= "Met at position OTHER INFORMATION: represents fmet"
                                                                                  NAME/KEY: misc_feature LOCATION: 146..148
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ZIP: 20007-5109
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                            202)672-5300
(202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sheila Garven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eva Walczyk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawrence T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phyllis Krygsman
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146..1756
sig_peptide
146..262
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Sequence 1, Application Us/09105537A
Patent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
CURRENT: APPLICATION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 15872
TYPE: DNA
ORGANISM: Streptomyces venezuelae
US-09-105-537-1
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; LOCATION:
US-08-951-742-1
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                                                                                                                                                Query Match
Best Local Similarity
Matches 172; Conserv
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Best Local Similarity 46.7%;
Matches 185; Conservative
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aaggacctgcggctcgacgccttcgtcctcttctcctccgtctccggcatcgtcggcacc
                   acgggccgctggaatgccgcctacgacatctggttcagtcccgtcacgaattccggcaac 1168
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263..1756
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Pred. No. 0.038;
0; Mismatches 208;
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                                                                                                                                                                Score 46.8; DB 4; Pred. No. 0.074;
                                                                                                                                                Mismatches
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                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                     Matches 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: DELLAPOR
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 0546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEPEX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FR PC COMPUTER: PC-DOS/MS-DOS
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1340 gtgagcgagctggacctgaaggccttcatcgacgacgcggtcgcccgcgggctacatcc 1397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7946 ctcaccccgctgcagggcctcgcgctcttcgacgccgcggtcgccagggacgacgccc
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                                        399
                                                                                                                                     TELEFAX: (20-
TELEFAX: 706141
929 ctggaaacgggcaacttcacgatcacacgggccgatcacgacaacggccaacaacgtggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/440,856A FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 20037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                           gactgggactggaattacatcgcctacc-----ggcgcacgacgcccaccacgtcg 1339
                                        GTCRGSTTCGTGCGSTGCGACGTGTCSGTGGAGGASGACGTSSRGCGCGCCGTSGACTGS 458
                                                                                                              GTGATCGCGGACATCGACGCGCGCGGGGGGGGGCGCTGGCGCCTGGGGSCCGCAS
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                                                                                                                                                                                                                                                                                                                                                                    1288 base pairs
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2000 PENNSYLVANIA AVE. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                    both
                                                                                                                                                                                   2.5%; Score 46.2; DB 1; 38.5%; Pred. No. 0.059; ative 48; Mismatches 346;
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MATERIALS AND METHODS FOR PRODUCING
PLANTS WITH SINGLE-SEX FLOWERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08804227C Patent No. 5876991
                                                                           ATTORNEY AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                               TELEPHONE: 317-276-24 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804;
FILING DATE: February 21, 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1169
                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SY
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1109
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                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: 15m. MS-DUS
OPERATING SYSTEM: MS-DUS
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CITY: INDIANAPOLIS
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ZIP: 46285
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       44377
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LILLY CORPORATE CENTER
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IBM Compatible
SYSTEM: MS-DOS
base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/804,227C
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                  APPLICANT: Burgett, Stanley G.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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TOPOLOGY: lin
MOLECULE TYPE: |
FEATURE:
                               COMPUTER: Macintosh OPERATING SYSTEM: Macintosh SOTTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
                                                                                           ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: FEATURE:
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                                                                                                                                                    COUNTRY:
                                                                                                                                                                                    STREET: LILLY CORPORTS CITY: INDIANAPOLIS
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APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                       STATE:
                                                                                                                                                                                                     ADDRESSEE: PAUL R. CANTRELL 1:
STREET: LILLY CORPORATE CENTER
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36155..41830
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31329..36071
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20110..31284
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350..14002
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47.6%;
               US/08/804,198
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Pred. No. 0.
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FEATURE:
NAME/KEY:
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COCATION:
US-08-804-198-1
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ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                       Ouery Match 2.5%; Score 46; DB 2; Length 44377; Best Local Similarity 47.6%; Pred. No. 0.14; Matches 136; Conservative 0; Mismatches 150; Indels
18728 GGGACCGCCCTGCCCACCAGCAGGAGATGGCGCACCTTGTGCCGG 18683
                                                                18848 GGGAGTGCGTCGAGCAGGCGCGCAGGGCGTCGCGGTCCGTGACGTCACAGGCCCCGTAC 18789
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NAME/KEY:
LOCATION:
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LOCATION:
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36155..41830
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31329..36071
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20110..31284
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14046..20036
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350..14002
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Gaps

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Search completed: August 19, 2002, 13:28:03 Job time: 12887 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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  50.60.8
557.2
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CNS0091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence. AL053013 AL053013.1 GI:4934461

ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL

SOURCE ORGANISM

fruit fly.

KEYWORDS

ACCESSION VERSION

COMMENT

Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr Genoscope. Direct Submission (bases 1 to 925)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

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/organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_lib="RPCI-98"

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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

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125; Conservative
                                                                                                                                         Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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           Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                                                                                     GSS
                                                                           Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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/db_xref="taxon:7227"
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45; Conserv
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                                                                                                                                                                                                                                                            CNS0072Q 932 bp DNA linear GSS 03-JUN-19 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
    Direct Sul
Submitted
                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 932)
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/db_xref="taxon:7227"
/db_ref="RPCI-98"
/clone="BACR19D16"
/clone="BACR19D16"
/note="end: TET3"
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CNS0072Q
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr)
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruittly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be constructed by the content of t
CSCSMSCCCCCGCASCV
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                                                       ggcgactgagcgacgca 642
                                                                                                                            SCGCCCCYGSCCSGGSCSSCCGCCMCMVARMAVSVSCCCCCCSCCMASCCCCGCVSGCSC
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 932)
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/db_xref="taxon:7227"
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Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library Unpublished (2001)

On Nov 16, 2000 this sequence version replaced gi:11182980.

Contact: Wing RA
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
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Total hq bases = 333
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
                                                  http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Al see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchors resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)*a 260 c 271 g 161 t
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HVcDNA0007 (Etiolated and unstressed)"
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                                                                                                                              Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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           /clone_lib="RPCI-98"
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                                                                                                             fly), gen
AL098882
                                                                                                                                                                                                                                                                          Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fi
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1009)
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/organism="Drosophila
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDC The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 844)
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Drosophila melanogaster genome sur
BACR11P16 of RPCI-98 library from
                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                              Genoscope.
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rom Drosophila melanogaster (fruit
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RESULT 1 CNS006XK LOCUS

DEFINITION

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Drosophila melanogaster genome surBACR14N09 of RPCI-98 library from flv), genomic survey sequence.

survey sequence rom Drosophila me

melanogaster T7 end of BAC

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ACCESSION VERSION

fly), genomi AL066051 AL066051.1

GI:4945019

SOURCE

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)

Insecta;

KEYWORDS

GSS fruit fly.

REFERENCE

AUTHORS TITLE

Genoscope.
Direct Submission

JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:

National de Sequencage segref@genoscope.

www.genoscope.cns.fr)

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AAAAGGBKKGGKGKDGKGKGGGGGGGGGGTTH
                                                                               VNGSVSGRBNNKYKTKTKTRKBKTBTKKKBGKABWKKTKKKKWTRKYKKTWRKGARAAAD
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR11P16"
/note="end : TET3"
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Pan troglodytes DNA, cloi
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GSS; GSS (genome survey :
Pan troglodytes male lym
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          GSS (genome survey sequence).
troglodytes male lymphoblast DNA,
Library clone:PTB-052M02.F.
troglodytes
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/db_xref="taxon:7227"
/db_xref="RPCI-98"
/clone="BACR14N09"
/clone="BACR14N09"
/note="end : T7"
170 c 162 g 96 t 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC en was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Mammalia; Eutheria;
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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/db_xref="taxon:9598"
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/sex="male"
/sex="male" lymphoblast"
/ceil_type="lymphoblast"
/clone_lib="prB Chimpanzee Male B#
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Pred. No. 9.2;
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Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
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BAC
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GSS; GSS (genome survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG060149 700 bp DNA linear GSS 03-NOV-200 Pan troglodytes DNA, clone: PTB-047122.R, genomic survey sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee
Library clone:PTB-047122.R.
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R.Site 2
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/clone_lib="PTB Chimpanzee Male
291 c 334 g 15 t
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/clone="PTB-047122.R"
/sex="male"
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Local Similarity 46.7%;
les 188; Conservative
                                                       ccggcgcgacaacgtgaagtggcgagcgcctggcctctgggcgctggccaacgactacgg
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4400 Fifth Avenue, Pittsburgh,
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Dept. Biol. Sci.
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Development 128 (13), 26
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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BG785566.1
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                                                                                                                                                                                                                                                                                                                                                                   Email: ettensohn@andrew.cmu.edu
Location/Qualiflers
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                                                                                                                                                                                                                                                                                       /organism="Strongylocentrotus
/db_xref="taxon:7668"
/clone="PC_0026_A1_G09_MR"
/clone_lib="Sea urchin primary
                                                                                                                                                                                                                               /cell_type="primary mesenchyme
/lab_host="E.coli"
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,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
Scara,G., Wheeler,M. and Zepeda,G.R.
Functional Genomics of Plant Stress Tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE040131 1022 bp mRNA OD102C08 OD Oryza sativa cDNA 5' similar transcription factors, mRNA sequence.
                                                                                                         . Similarity
99; Conser
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Fax: 520-621-1697
                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                       Email: cbm@u.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Michalowski, C.B.
                                                                                                                                                                                                                                                                                                                                                                                          University of Arizona
                                                                                                                                                                                                                                                                                                          open reading frame exists
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 1022)
                                                                                                                                                                                       196
                                                                                                         Conservative
                                                                                                                                                                               /organism="Oryza sativa"
/strain="Pokkali"
/db_xref="taxon:4530"
/clone_lib="OD"
/tissue_type="roots"
/dev_stage="1 week"
/note="1 d 150mm NaCl"
285 c 292 g 217
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0; Mismatches
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Best Local Similarity 44.0%;
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                                                                                   gagaccgcccagtgcattgaggtcggactggaaacggggcaacttcacgatcacacgggcc 961
                                                                                                                       CCGGGGGGGGGGGGACAGACGGGCGACACAGGGAGCAAAAGGACAAACAGTGGGTTGGC 262
                                                                                                                                       GGTCGCCNCGGCCGCGGCCCCGCGCGCGCGCGCCCCGCGGCCAGGGCGAACGCGAC
                                                                                                                                                                                                                                               307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS; GSS (genome survey sequence). Pan troglodytes male lymphoblast DNA, BAC Library clone:PTB-047K07.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama,A., Hattori,M., Toyoda,A., '
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes DNA, cla
AG060214
AG060214.1 GI:16611446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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R.Site 2
                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tracking errors.
                                                                                                                                                                                                                                                                                                                                    /clone="PTB-047K07.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
/clone_lib="PTB Chimpanzee Male
                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Primates;
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PTB-047K07.F,
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26 others
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genomic
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Search completed: August 19, 2002, 10:59:49 Job time: 4368 sec

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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being put and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen
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ALIGNMENTS

RESULTATION (NATIONAL PROTEIN; 260 ID AAY06369 standard; Protein; 260

XX PD 4.4324 ⊋JUN.∋1999. SXXXXX Rhodothermus marinus. Cellulase; endoglucanase; EGIII; textile; Rhodothermus marinus EGIII-like cellulase 06-SEP-1999 Bower BS, (GEMV) GENENCOR INT INC 14-DEC-1998; food processing; grain 16-DEC-1997; Fowler T, (first entry) 97US-0991720 98WO-US26552. Phillips JI; wet milling; pulp; paper. feed additive; baking;

Result No.

Score

Query Match

Length

DВ

IJ

Description

AAY06369 AAB14882 AAY84347

1318. 1318. 1470. 400. 396.5 396.5 396.5 396.5

21 21 21 21

AAY06342 AAY67497 AAY06367 AAY08473 AAB14880 AAY84345 AAY67496 AAY06368

Protien sequence o Streptomyces sp. E Actinomycete sp. 3 Streptomyces livid Amino acid sequenc Actinomycetes cell

The present polypeptide represents a full-length sequence

of.

Example; Fig 6; 47pp; English.

EGIII like cellulase WPI; 1999-395187/33.

Amino acid sequenc Rhodothermus marin Rhodothermus marin Emericella deserto

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Best Local S
Matches 241
                                                                                                                                                                                                 cellulase;
wood pulp :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               novel EGIII-like cellulase of Rhodothermus marinus. It was deduced from a gene sequence isolated from genomic DNA using PCR primers (see AAX59180-91) based on conserved motifs (see AAY06325-29) of Trichoderma reesel EGIII cellulase and related enzymes. PCR has been used to identify novel EGIII-like enzymes, including the present protein, from bacterial and fungal sources (see AAY06331-70). The sequence shows homology to T. reesel EGIII (see AAY06330). Also provided by the invention are vectors, host cells and methods for the recombinant production of such enzymes, which can be used in the treatment of cellulose-containing textiles, as feed additives, in the treatment of wood pulp, in the reduction of biomass to glucose, in the stone washing of indigo dyed denim, or as laundry detergent components (all claimed).
Novel endoglucanase
                                                                                       18-DEC-1998;
                                                                                                             12-NOV-1999;
                                                                                                                                   29-JUN-2000
                                                                                                                                                         WO200037614-A2
                                                                                                                                                                             Emericella desertoru.
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                                                                                                                                                                                                                                                                     21-NOV-2000
                                                                                                                                                                                                                                                                                          AAB14882;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                (GEMV ) GENENCOR INT INC
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                     2000-482483/42
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241; Conserv
                                                                                                                                                                                                   treatment;
                                           ú
                                                                                                                                                                                                           desertoru; Trichoderma reesei; endoglucanase III; EGIII;
mutant; enzyme stability; textile treatment;
                                                                                                                                                                                                                                              desertoru
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                                                                                                             99WO-US26704
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t; feed
III
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or endoglucanase III-like
                                                                                                                                                                                                   stability;
additive;
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Pred. No. 1.7e-118;
4; Mismatches 9;
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cellulase
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useful
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for
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The present sequence is a cellulase related to endoglucanase III (EGIII) from Trichoderma reesei. EGIII-like genes were isolated from genomic DNA libraries constructed from various microorganisms by PCR. The isolated genes showed significant homology to EGIII from T. reesei. Certain subsitution and deletion mutations have been incorporated into EGIII and EGIII-like cellulases to produce variant enzymes with improved stability, e.g. increased resistance to temperature stress. The mutants may be used in textile and wood pulp treatment, as a feed additive, and for reducing biomass to glucose. They are also useful for stonewashing or indigo dyed denim and as an agent in laundry and dish detergents.
                                                                                                                                                                                                                                                                                                                                        specified positions in the wild
                                                                                                                                                                                                                                                                                           Fig
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                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                        comprises a substitution or deletion form of endoglucanase III \,
                                                                                                                                                                                                                                                                                                                                                                   at
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Sequence

260

A,

DB

21;

Length

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RESULT
AAY84347-
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 241
cellulase; textile processing; textile cleaning; stonewasning; indigo dyed denim; cellulose containing fabric; fabric smoothness; pill removal; fibril removal; cotton; cellulosic fibre; dying; det animal feed: wood pulp; paper; grain; biomass reduction; glucose.
                                                Endoglucanase III; EGIII; EGIII-like cellulase; surfactant
                                                                       Amino acid
                                                                                                                        AAY84347;
                                                                                                                                              AAY84347
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                                                                                                                                                                                                                                                                                                  VWGAETAQCIEVGLETGNFTITRADHDNGNNVAAYPAIYFGCHWGA-----CTSNSGLP 114
                                                                                                                                                                                                        lhavetgfelweggaglrtadfsvtvq
                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
241; Conserv
                                                                                                                                               standard;
                                                                         sequence of an endoglucanase III (EGIII)-like cellulase.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                (first
                                                                                                                                               Protein;
                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1318.5; DB
Pred. No. 1.7e-11
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
9;
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Rhodothermus

marinus.

detergent;

A CONTRACTOR

03-SEP-1998; 24-AUG-1999; 16-MAR-2000. WO200014208-A1.

98US-0146729 99WO-US19154

(GEMV) GENENCOR INT

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RAYOGAY
AAYOGAY
ID AAYO
XX AAYO
XX AAYO
XX CPI
DT 06-5
XX Rhod
XX Gell
KW Good
XX Fhod
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an endoglucanase III (EGIII)-like cellulase. The cellulase has homology to the Trichoderma reesei EGIII protein. The variant cellulases have improved temperature stability, and improved surfactant stability. The variant cellulases and compositions containing them are used in textile processing or cleaning, e.g. stonewashing of indigo dyed denim, and modifying the texture, feel or appearance of cellulose containing fabrics (e.g. improving fabric smoothness or removing pills and fibrils). The compositions may also be used for the removal of immature or dead cotton from cellulosic fibres or fabric, which can cause uneven dying. The cellulase may also be used in a detergent composition for washing laundry and dishes and in the treatment of animal feed, wood pulp, paper, non-animal foods and grains. The enzymes may also be used in the reduction of biomass to glucose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel variant endoglucanase III-like cellulases with improved surfactant stability and resistance to temperature stress, useful for textile processing or cleaning, treating wood pulp, food and grain, and reducing biomass to glucose
                14-DEC-1998;
                                                                                                          Rhodothermus marinus
                                                                                                                                      Cellulase; endoglucanase; EGIII; textile; food processing; grain wet milling; pulp;
                                                                                                                                                                                     Rhodothermus marinus EGIII-like cellulase (partial sequence)
                                                                                                                                                                                                                                                                                   AAY06342 standard; Protein; 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-271052/23
                                                                              WO9931255-A2
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                                                                                                                                                                                                                                                                                                                                                           RRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNWNGGVMPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDLKAFIDDAVARGYIRPEWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rraheld-----vtpittgrwnaaydiwfspvtnsgngysggaelmiwlnwnggvmpg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNVMRAVLVLSLLLLEGCDWLFPDGDNGKEPEPEPEPTVELCGRWDARDVAGGRYRVINN 60
                                                                                                                                                                                                                                                                                                                                                                                                                         gsrvatvelagatwevwyadwdwnyiayrrttpttsvseldlkafiddavargyirpewy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 66-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                     (first entry)
                  98WO-US26552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191.28; Score 1318.5; DB 2
90.38; Pred. No. 1.7e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                         paper
                                                                                                                                                        feed additive; baking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                           233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
24-JUN-1998;
18-NOV-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present polypeptide represents a partial sequence of a novel EGIII-like cellulase of Rhodothermus marinus. It was deduced from a partial gene sequence isolated from genomic DNA using PCR primers (see AAX59180-91) based on conserved motifs (see AAX06325-29) of Trichoderma reesei EGIII cellulase and related enzymes. PCR has been used to identify novel EGIII-like enzymes, including the present polypeptide, from bacterial and fungal sources (see AAX06331-70). Also provided by the invention are vectors, host cells and methods for the recombinant production of such enzymes, which can be used in the treatment of cellulose-containing textiles, as feed additives, in the treatment of vood pulp, in the reduction of biomass to glucose, in the stone washing of indigo dyed denim, or as laundry detergent components (all claimed).
                                                28-MAY-1999;
                                                                                                                                        Protein
                                                                                                                                                                            Кеу
                                                                                                                                                                                                   Streptomyces lividans Synthetic.
                                                                                                                                                                                                                                                    Cellulase; Actinomycetes; detergent; feed additive; textile treatment;
                                                                                                                                                                                                                                                                                                                              AAY67497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-395187/33
                                                                           24-FEB-2000.
                                                                                                   WO200009707-A1
                                                                                                                                                               Peptide
                                                                                                                                                                                                                                        pulp; paper;
                                                                                                                                                                                                                                                                             Protien sequence of CelA and cellulase 11AG8 fusion
                                                                                                                                                                                                                                                                                                      19-MAY-2000
                                                                                                                                                                                                                                                                                                                                                        AAY67497 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGIII like cellulase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bower BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMV ) GENENCOR INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                 113 LPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIW 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 avrraheld-----vtpittgrwnaaydiwfspvtnsgngysggaelmiw
                                                                                                                                                                                                                                                                                                                                                                                G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fowler T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; 47pp;
                                                                                                                                                                                                                                        cellulase 11AG8
98US-0104308.
98WO-US24649.
99US-0321981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0991720.
                                                  99WO-US11971
                                                                                                                                         /note=
47..386
                                                                                                                                                                          Location/Qualifiers
                                                                                                                                         386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phillips JI;
                                                                                                                          "cellulase 11AG8 mature peptide"
                                                                                                                                                 _"celA signal sequence"
                                                                                                                                                                                                                                                                                                                                                        386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 470.5; DB 20;
Pred. No. 1.5e-37;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105;
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RESULT
AAYOG367
ID AAYC
XX AAYC
AC AAYC
XX Stre
DT 06-S
CXX Cell
KW Cell
KW Food
XX Gel
XX WO99
PN WO99
XX 14-I
PF 14-I
XX BOWE
XX BOW
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                                                                                                                                                                                                                                                                           14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9931255-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cellulase; endoglucanase; EGIII; textile; food processing; grain wet milling; pulp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A novel Actinomocyes cellulase and recompositions, treating textiles and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-224344/19.
N-PSDB; AAZ57031.
                                                                                                                     (GEMV ) GENENCOR INT
                                                                                                                                                                                                  16-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                           24-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
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Pred. No. 4.3e-30;
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24-JUN-1998; 19-NOV-1997; 19-NOV-1997;

98US-0104308. 97US-0974041. 97US-0974042. WO9925846-A2 27-MAY-1999.

18-NOV-1998;

98WO-US24649

Cellulase; detergent; animal feed; nutritional value; textile; stone washing; texture modification; appearance; cellulosic fabric; pulp; draining; papear; baking additive; starch treatment; grain; high-fructose corn syrup production; ethanol production; fibre reduction;

Actinomycete sp. 36kD cellulase protein

AAY08473; 28-JUL-1999

(first entry)

milling.
Actinomyces

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The present polypeptide represents a full-length sequence of a novel EGIII-like cellulase of Streptomyces sp. 11AG8. It was deduced from a gene sequence isolated from genomic DNA using PCR primers (see AAX59180-91) based on conserved motifs (see AAY06325-29) of Trichoderma reesei EGIII cellulase and related enzymes. PCR has been used to identify novel EGIII-like enzymes, including the present protein, from bacterial and fungal sources (see AAY06331-70). The sequence shows homology to T. reesei EGIII (see AAY06331). Also provided by the invention are vectors, host cells and methods for the recombinant production of such enzymes, which can be used in the treatment of cellulose-containing textiles, as feed additives, in the treatment of wood pulp, in the radiction of biomass to glucose, in the stone washing of indigo dyed denim, or as laundry detergent components (all claimed).
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Best Local S
Matches 89
AAY08473 standard; Protein;
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                                                                                        kdfvdqavshglatpdwyltsiqagfepweggtglavnsfssav
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39.7%;
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Pred. No. 1e
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Best Local S
Matches 89
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            Mitchinson C,
                                                                                                                                                                               Streptomyces lividans
                                                                                                                                                                                                                      Streptomyces lividans; Trichoderma reesei; endoglucanase cellulase; mutant; enzyme stability; textile treatment;
                                                                                                                                                                                                                                                               Streptomyces lividans CelB EGIII-like cellulase
                                                                                                                                                                                                                                                                                                                                                 AAB14880 standard; Protein; 371
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N-PSDB; AAV72359.
                                                                   18-DEC-1998;
                                                                                             12-NOV-1999;
                                                                                                                                                                                                         wood pulp treatment;
                                                                                                                                                                                                                                                                                           21-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     improve draining) and paper. They may also be used as baking additives, for treating starch (in production of high-fructose corn syrup or ethanol) and for treating grain (to reduce fibre during milling).
                                        (GEMV ) GENENCOR INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 ELCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGN-FTITRADHDNGNNVA--AYP 96
                                                                                                                                                                                                                                                                                                                                                                            œ
                                                                                                                                                                                                                                                                                                                                                                                                                  kdfvdqavshglatpdwyltsiqagfepweggtglavnsfssav
                                                                                                                                                                                                                                                                                                                                                                                                                                               KAFIDDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -rteimiwfnrvgpvqpigspvgtahvggrswevwtgsngsndvisflapsaisswsfdv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATYFGCHWGACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYS. 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              svydgchygncaprttlpmrissigsapssvsyrytgngvynaaydiwldp-tprtngvn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Der Kleij
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
            Wendt DJ;
                                                                   98US-0216295
                                                                                             99WO-US26704
                                                                                                                                                                                                           enzyme
t; feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WAH,
                                                                                                                                                                                                        stability; textile t
additive; detergent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 396.5; DB Pred. No. 1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in detergent compositions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sollingen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weyler
                                                                                                                                                                                                                                                                                                                                                                                                                     251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Σ
                                                                                                                                                                                                                                     III; EGIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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The present sequence is a cellulase related to endoglucanase III (EGIII) from Trichoderma reesei. EGIII-like genes were isolated from genomic DNA libraries constructed from various microorganisms by PCR. The isolated genes showed significant homology to EGIII from T. reesei. Certain subsitution and deletion mutations have been incorporated into EGIII and EGIII-like cellulases to produce variant enzymes with improved stability, e.g. increased resistance to temperature stress. The mutants may be used in textile and wood pulp treatment, as a feed additive, and for reducing biomass to glucose. They are also useful for stonewashing or indigo dyed
                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel endoglucanase III or endoglucanase III-like cellulase useful for treating textiles and wood pulp comprises a substitution or deletion at specified positions in the wild form of endoglucanase III \, -
                                                                         Sequence
                                                                                                                   in textile and wood pulp treatment, as a feed additive, ar
biomass to glucose. They are also useful for stonewashing
denim and as an agent in laundry and dish detergents.
                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 3; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-482483/42
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                                                                              B
  DВ
21;
Length
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RRESULT
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XX AAMin
XX Endc
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endoglucanase III; EGIII; EGIII-like cellulase; surfactant stability; cellulase; textile processing; textile cleaning; stonewashing; indigo dyed denim; cellulose containing fabric; fabric smoothness; pill removal; fibril removal; cotton; cellulosic fibre; dying; deterganimal feed; wood pulp; paper; grain; biomass reduction; glucose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200014208-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomyces sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of an endoglucanase III (EGIII)-like cellulase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY84345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY84345 standard; Protein; 371 AA
                                                                                                                                                                                                                                                                                                                                                                 16-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIYFGCHWGACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qicdrygtttiq-dryvvqnnrwgtsatqcinv---tgngfeitqadgsvptngapksyp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               svydgchygncaprttlpmrissigsapssvsyrytgngvynaaydiwldp-tprtngvn 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99;
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(GEMV) GENENCOR INT INC

03-SEP-1998; 24-AUG-1999;

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Best L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents an endoglucanase III (EGIII)-like cellulase. The cellulase has homology to the Trichoderma reesei EGII protein. The variant cellulases have improved temperature stability, and improved surfactant stability. The variant collulation is a sequence of the collulation of
     28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cellulase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200009707-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pulp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetes cellulase protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY67496 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 64-65; 73pp; English.
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89; Conservative
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     99WO-US11971
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28..372
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39.78;
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Pred. No. 1e-29;
Pred. No. 1e-29;
                                                                                                                                                                                                                                                                                                                                                                                    sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EGIII)-like
erma reesei EGIII
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Best Local Similarity
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18-NOV-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be used in a detergent composition, as an additive for animal feed and for the treatment of textiles or pulp and paper. The DNA encoding the cellulase can be used to identify homologous cellulases and for recombinant production of cellulases. The present sequence represents cellulase from Actinomycetes.
                                16-DEC-1997;
                                                                                                                                                                                                        06-SEP-1999
                                                                                                                                                                                                                                                    AAY06368 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A novel Actinomocyes cellulase and related DNA, useful for compositions, treating textiles and paper or pulp
         (GEMV ) GENENCOR INT INC
                                                      14-DEC-1998;
                                                                              24-JUN-1999.
                                                                                                    WO9931255-A2
                                                                                                                         Streptomyces lividans
                                                                                                                                                                                 Streptomyces lividans EGIII-like cellulase
                                                                                                                                                                                                                                AAY06368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones BE,
                                                                                                                                                food processing;
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                                                                                                                                                                                                                                                                                                                                    217
                                                                                                                                                                                                                                                                                                                                                         149
                                                                                                                                                                                                                                                                                                             208 kdfvdqavshglatpdwyltsiqagfepweggtglavnsfssav 251
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                                                                                                                                                                                                                                                                                                                                                                                                                          97 AIYFGCHWGACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                34 gicdrygtttig-dryvvqnnrwgtsatqcinv---tgngfeitgadgsvptngapksyp
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                                                                                                                                                                                                                                                                                                                         KAFIDDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTV
                                                                                                                                                                                                                                                                                                                                                        -rteimiwfnrvgpvqpigspvgtahvggrswevwtgsngsndvisflapsaisswsfdv
                                                                                                                                                                                                                                                                                                                                                                               GGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDL
                                                                                                                                                                                                                                                                                                                                                                                                    svydgchygncaprttlpmrissigsapssvsyrytgngvynaaydiwldp
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DB; AAZ57029.
                                                                                                                                                          endoglucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Der Kleij WAH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       provides a cellulase from Actinomycetes. The cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0104308.
98WO-US24649.
99US-0321981.
                                97US-0991720
                                                       98WO-US26552
                                                                                                                                              grain wet milling;
                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.4%;
                                                                                                                                                            EGIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 396.5; DB Pred. No. 1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Solingen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                          textile;
                                                                                                                                                pulp; paper
                                                                                                                                                             feed additive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                            baking;
                                                                                                                                                                                                                                                                                                                                                                                                      -tprtngvn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cellulase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detergent
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ARESULT 12
AAB14881
ID AAB148
AC AAB
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Best Local S
Matches 77
                                            (GEMV ) GENENCOR INT INC
                                                                                                                         18-DEC-1998;
                                                                                                                                                                                                  12-NOV-1999;
                                                                                                                                                                                                                                                                               29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhodothermus marinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wood pulp treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cellulase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodothermus marinus; Trichoderma reesei; endoglucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodothermus marinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 tdlpvrldtvsaapssisygfvdgavynasydiwldptartdg--vnqteimiwfnrvgp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 ndwyltsvqagfepwqngaglavnsfsstve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 PEWYLHAVETGFELWEGGAGLRSADFSVTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDLKAFIDDAVARGYIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant; enzyme stability;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                     98US-0216295
                                                                                                                                                                                                  99WO-US26704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGIII-like cellulase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  feed additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phillips JI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
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Pred. No. 1.4e-24;
1; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detergent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               III; EGIII;
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cellulase; textile processing; textile cleaning; stonewashing; indigo dyed denim; cellulose containing fabric; fabric smoothness; pill removal; fibril removal; cotton; cellulosic fibre; dying; det

detergent;

Endoglucanase III; EGIII; EGIII-like cellulase; surfactant stability; Amino acid sequence of an endoglucanase III (EGIII)-like cellulase 12-JUL-2000 AAY84346

(first entry)

animal feed; wood pulp; paper; grain; biomass reduction; glucose.

Streptomyces lividans.

03-SEP-1998; 24-AUG-1999; 16-MAR-2000. WO200014208-A1

98US-0146729 99WO-US19154

(GEMV) GENENCOR INT

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RESULT 1
AAY84346
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel endoglucanase III or endoglucanase III-like cellulase useful for treating textiles and wood pulp comprises a substitution or deletion specified positions in the wild form of endoglucanase III -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitchinson C,
                                                                                                                                                                                                                                                                                                                                                                         AAY84346 standard; Protein; 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 SGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNWNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ប្រ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 GRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVA--AYPAIYFGCHWGACTSN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDLKAFIDDAVARGYIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ndwyltsvqagfepwqngaglavnsfsstve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEWYLHAVETGFELWEGGAGLRSADFSVTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iqpigspvgtasvggrtwevwsggngsndvlsfvapsaisgwsfdvmdfvratvarglae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tdlpvrldtvsaapssisygfvdgavynasydiwldptartdg--vnqteimiwfnrvgp 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gryvvqnnrwgstapqcv-tatdtg-frvtqadgsaptngapksypsvfngchytncspg 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 3; 52pp; English.
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36.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 343; DB 21;
Pred. No. 1.4e-24;
1; Mismatches 97
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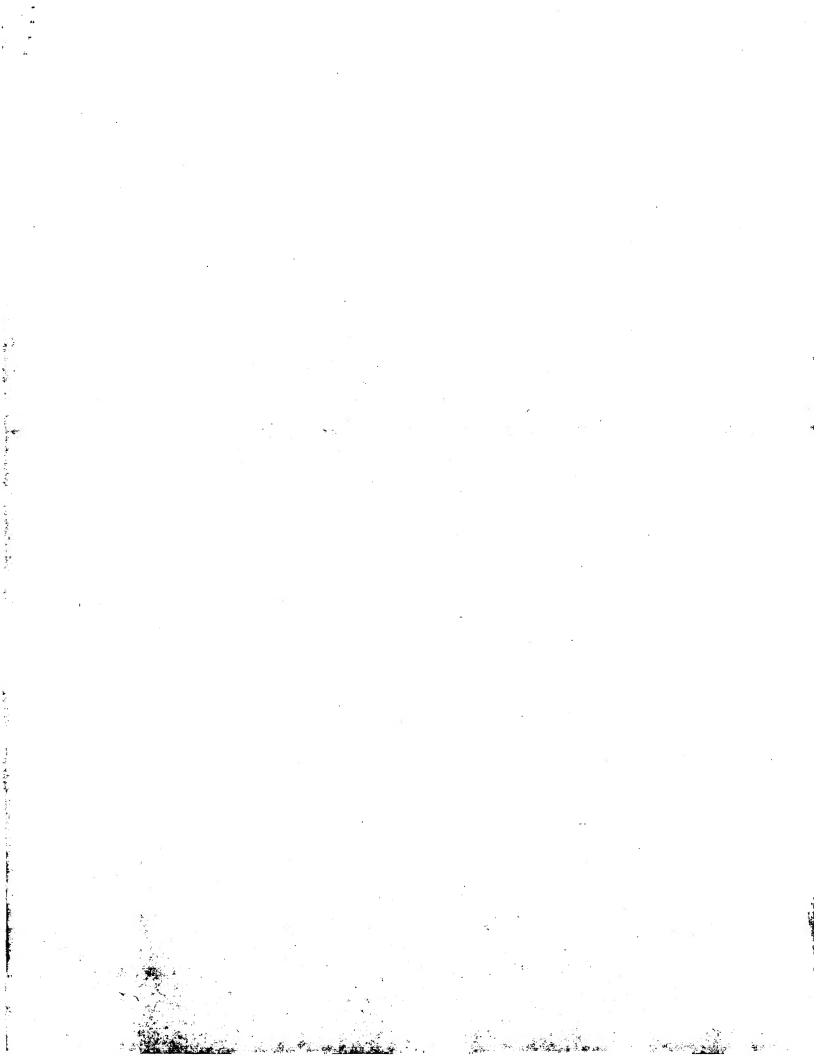
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AAW88462
ID AAW8
XX AAW8
XX AAW8
XX AAW8
XX Bacd
XX Xylc
XX SBacd
XX Xylc
XX Bacd
XX Ylc
XX WO91
FT Prot
FT
XX WO91
XX WO91
XX O1-4
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents an endoglucanase III (EGIII)-like cellulase. The cellulase has homology to the Trichodorma reesei EGIII protein. The variant cellulases have improved temperature stability, and improved surfactant stability. The variant cellulases and compositions containing them are used in textile processing or cleaning, e.g. stonewashing of indigo dyed denim, and modifying the texture, feel or appearance of cellulose containing fabrics (e.g. improving fabric smoothness or removing pills and fibrils). The compositions may also be used for the removal of immature or dead cotton from cellulosic fibres or fabric, which can cause uneven dying. The cellulase may also be used in a detergent composition for washing laundry and dishes and in the treatment of animal feed, wood pulp, paper, non-animal foods and grains. The enzymes may also be used in the reduction of biomass to glucose.
01-JUL-1998;
                                  21-JAN-1999
                                                                                                                            Protein
                                                                                                                                                                          Bacillus
                                                                                                                                                                                                                                     Bacillus licheniformis xyloglucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel variant endoglucanase III-like cellulases with improved surfactant stability and resistance to temperature stress, useful for textile processing or cleaning, treating wood pulp, food and grain, arreducing blomass to glucose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                              WO9902663-A1
                                                                                                                                                                                                                                                                      10-MAY-1999
                                                                                                                                                                                                                                                                                                     AAW88462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                         Xyloglucanase;
                                                                                                                                                                                                                                                                                                                                   AAW88462 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reducing biomass to
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                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                          {\tt sfvapsalsgwsfdvmdfvratvarglaendwyltsvqagfepwqngaglavnsfsstve}
                                                                                                                                                                                                                                                                                                                                                                                                                             YRRTTPTTSVSELDLKAFIDDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diwldptartdg--vnqteimiwfnrvgpiqpigspvgtasvggrtwevwsggngsndvl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIWESPYTNSGNGYSGGAELMIWLNWNGGYMPGGSRVATVELAGATWEVWYADWDWNYIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 32.979; Conservative
                                                                                                                                                                            licheniformis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 65-66; 73pp; English.
                                                                                                                                                                                                                                                                     (first entry)
98WO-DK00290
                                                                                                                                                                                                      detergent
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                                                                                                                           Location/Qualifiers 30..261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.98;
                                                                                             "mature protein, this region claimed in Claim 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                                                                                                   261
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Pred. No. 2.7e-23;
34; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                   B
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                                                                                                                                                                                                                                                                                                                                                                                                                                        This polypeptide is an alkaline xyloglucanase obtained from Bacillus licheniformis ATCC 14580. The enzyme shows optimal activity at 60 deg C, and rectains 50% of its activity affer 20 min at 70 deg. The optimum pH for activity is 5.54, with 32% relative at 70 deg. The optimum pH for activity is 5.54, with 32% relative activity retained at pH 4.59, and 45% at pH 8.49. The keat is 16.5/sec on xyloglucan at pH 7.5, Km 1.1 g/l. The ratio of maximum xyloglucanase activity to maximum activity on CM-cellulose is at cleast 5:1. An isolated polynucleotide (see AAX06949) encoding the xyloglucanase can be utilised in the production of recombinant enzyme. Xyloglucanase preparations are useful for improving the properties of cellulosic fibres, yarn, (non)woven fabric, and for rating hemp, jute, flax and linen fibres (claimed). They can also detergent compositions (claimed). The enzyme preparations exhibit high xyloglucanase activity at alkaline pH without essentially cattacking cellulose or cellulose derivatives.
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New enzyme preparation comprising a xyloglucanase with an activity of 50 % at pH 7 - useful for improving the properties of cellulosic fibres, yarn, (non)woven fabric, and ratting hemp, jute, flax and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-1997;
07-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 29; Page 71-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bjornvad ME,
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linen fibres
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  213
                                                                                                                  160
                                                                                                                                                                          101 GCHW-GACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGA 159
                                      214 LDLKAFIDD-AVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTVQ 261
                                                                            155
                                                                                                                                                        95
                                                                                                                                                                                                                                 45 kyyifnnvwgadqvsgwwqti-----yhnsdsdmgwvwnwpsntstvkaypsivs
                                                                                                                                                                                                                                                                       54 RYRVINNVWGAETA----QCIEVGLETGNFTITRAPHD------NGNNVAAYPAIYF 100
                                                                                                                ELMIWLNWNGGVMPGGSRVATVELAGATWEVW--YAD----WDWNYIAYRRTTPTTSVSE
                                                                                                                                                    gwhwtegytagsgfptrlsdqknintkvsysisangtynaaydiwlhntnkaswdsaptd 154
                                                                        eimiwln-ntnagpagsyvetvsigghswkvykgyidagggkgwnvfsfirtantqs-an
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lnirdftnyladskqwlsktkyvssvefgtevfggtgqinisnwdvtvr
                                                                                                                                                                                                                                                                                                             70;
                                                                                                                                                                                                                                                                                                           Similarity 30.670; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX06949
                                                                                                                                                                                                                                                                                                                                                                                                          261 AA;
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97DK-0000822
                                                                                                                                                                                                                                                                                                                               17.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PL,
                                                                                                                                                                                                                                                                                                         ; Score 255.5; DB 20; Pred. No. 2.2e-16; 41; Mismatches 85;
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                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                   261;
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RESULT 15
AAY06370
ID AAY06370;
XX
AC AAY06370;
XX
DT 06-SEP-1999 (first entry)
XX
DE Erwinia carotovora EGIII-like cellulase.
XX
Cellulase; endoglucanase; EGIII; textile; feed additive; baking;
XX
Cos Erwinia carotovora.
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WO9931255-A2

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Search completed: August 15, 2002, 10:51:03 Job time: 257 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The present polypeptide represents a full-length sequence of a covel ECIII-like cellulase of Erwinia carotovora. It was deduced from a gene sequence isolated from genomic DNA using PCR primers (see AAX59180-91) based on conserved motifs (see AAY06325-29) cof Trichoderma reesei ECIII cellulase and related enzymes. PCR has been used to identify novel ECIII-like enzymes, including the present protein, from bacterial and fungal sources (see AAY06331-70). The sequence shows homology to T. reesei ECIII (see AAY06330). Also provided by the invention are vectors, host cells and methods for the recombinant production of such enzymes, which can be used in the treatment of cellulase-containing textiles, as feed additives, in the treatment of wood pulp, in the reduction of biomass to glucose, in the stone washing of indigo dyed denim, or as laundry detergent components (all claimed).
                                                                                                                                                                                                                                                                                                                                                       Query Match 17.5%; Score 252.5; DB 20; Length 264; Best Local Similarity 31.6%; pred. No. 4.3e-16; Matches 72; Conservative 39; Mismatches 86; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Fig 6; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGIII like cellulase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-395187/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUN-1999
                                                                             163 IWLN-WNGGYMPGGSRVATVELAGATWEVWYADW------DWNYIAYRRTTPTTSVSEL 214
                                                                                                                                                                                                                101 wtagytensglpiqlssnksitsnvtysikatgtynaaydiwfhttdkanwdssptdelm 160
                                                                                                                                                                                                                                       104 WGA-CTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELM 162
                                                                                                                                                                                                                                                                                  54 RYRVINNVWGAETAQ------CIEVGLETGNFTITRADHDNGNNVAAYPAIYFGCH 103
                                                                                                                                                                                                                                                                                                                                                                                                                                            264 AA;
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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                     15-18-5 12-2

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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
386 4 US-09-2016-205-201 Sequence 23, Appli 312 4 US-09-104-395-21 Sequence 21, Appli 312 4 US-09-104-395-21 Sequence 21, Appli 371 4 US-09-104-395-21 Sequence 21, Appli 371 4 US-09-104-395-2 Sequence 22, Appli 371 4 US-09-216-295-2 Sequence 22, Appli 261 4 US-09-216-295-2 Sequence 22, Appli 273 1 US-08-032-848C-12 Sequence 24, Appli 273 1 US-08-032-848C-12 Sequence 27, Appli 273 4 US-09-216-295-7 Sequence 27, Appli 273 4 US-09-216-295-10 Sequence 17, Appli 273 4 US-09-216-295-10 Sequence 17, Appli 273 4 US-09-216-295-10 Sequence 17, Appli 273 4 US-09-216-295-13 Sequence 17, Appli 274 4 US-09-216-295-13 Sequence 17, Appli 275 4 US-09-216-295-13 Sequence 17, Appli 275 4 US-09-216-295-13 Sequence 17, Appli 275 4 US-09-216-295-13 Sequence 18, Appli 275 4 US-09-216-295-13 Sequence 19, Appli 275 4 US-09-216-295-13 Sequence 10, Appli 275 4 US-09-216-295-13 Sequence 10, Appli 275 4 US-09-216-295-13 Sequence 10, Appli 275 4 US-09-216-295-13 Sequence 21, Appli 275 4 US-09-216-295-13 Sequence 23, Appli 275 4 US-09-216-295-13 Sequence 24, Appli 275 4 US-09-216-295-13 Sequence 275 4 Appli 275 4 US-09-216-295-13 Seque
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RESULT 2
US-09-321-981-5
; Sequence 5, Application Uf
; Patent No. 6287839
; Patent No. 6287839

US/09321981

234

121 175 174

174 173

234

235 LHAVETGFELWEGGAGLRSADFSVTVQ 261

LHAVETGFELWEGGAGLRTADFSVTVQ

Query Match Best Local Sim Matches 241; Qy 1 MNVMRA' Db 1 MVMRAET. Qy 61 VWGAET. Db 61 VWGAET.	SEQUENCE 23 Application US/09216295 SEQUENCE 23 Application US/09216295 SELECTION OF 16568328 3 GENERAL INFORMATION: APPLICANT: Mitchinson, Colin APPLICANT: Mendt, Dan J. TITLE OF INVENTION, NO. 6268328el Var FILE REFERENCE: GC55 CURRENT APPLICATION NUMBER: US/09/216, CURRENT APPLICATION NUMBER: US/09/216, CURRENT SECTIONS: 41 NUMBER OF SECTIONS: 41 SOFTWARE: FastSEC for Windows Version SECTION OF S		28 176.5 29 17.2 30 166.5 31 166.5 32 166.5 33 166.5 34 163.5 35 163.5 36 163.5 37 162.5 39 161.5 40 159.5 41 159.5 42 141.5 43 141.5
Similarity 90. Similarity 90. 1; Conservative MRAVLVLSLLLLFGCD MRAVLVLSLLLLFGCD AETAQCIEVGLETGNF	-23 Application 626938 626938 Mitchinson, Mitchinson, Mitchinson, Mitchinson, MITCHINSON, NVENTION, NO. ENCE: GC555 PLICATION, NUMBER PLICATION, NUMBER PLICATION, NUMBER PLICATION, NUMBER PLICATION, NUMBER PLICATION, NUMBER PLICATION, NUMBER PLICATION, NUMBER PLICATION, NUMBER MITCHINSON, NUMBER MITCHINS		11.5 11.5 11.5 11.5 11.5 11.5 11.5 11.5
entive LFGCDWL LFGCDWL LFGCDWL LFGCDWL LFGCDWL LFGCDWL	ton US/0921 nn, Colin nn, Colin No. 626832 55 No. 626832 1938-12831 1938-12831 1957 Windows nus marinus		32888888888888888888888888888888888888
VLEE VLEE	7092 2683 30ws		444433433333333333333333333333333333333
Score 1318.5; DB 4; Pred. No. 1.1e-123; 4; Mismatches 9; I DGDNGKEPEPEPEPTVELCGRWD	→ A.U. (7) iant EGIII-Like 295 3.0	ALIGNMENTS	US-09-216-295-3 US-09-216-295-15 US-09-216-295-19 US-09-216-295-4 US-09-215-042-1 US-09-216-295-14 US-09-216-295-6 US-09-216-295-8 US-09-216-295-8 US-09-216-295-8 US-09-216-295-8 US-09-216-295-12 US-08-849-751-2 US-09-478-816-2 US-09-216-295-11 US-08-995-280C-2 US-09-215-042-2 US-09-215-042-2 US-09-215-042-2
Length 260; Indels 13; Gaps 2; DARDVAGGRYRVINN 60 DARDVAGGRYRVINN 60 ACTSNSGLP 114	S. Cellulase Compositions		Sequence 3, Appli Sequence 15, Appl Sequence 19, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

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US-09-216-295-21
; Sequence 21, Application US/09216295
; Patent No. 6268338
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OTHER INFORMATION: Nearest "neighbor" - Streptomycetes
OTHER INFORMATION: thermovebaceous
US-09-321-981-5
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US-09-216-295-21
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CURRENT APPLICATION NUMBER: US/09/321,981

CURRENT FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: PCT/US99/11971

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 09/104,308

PRIOR FILING DATE: 1998-06-24

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 08/974,042

PRIOR FILING DATE: 1997-11-19

PRIOR FILING DATE: 1997-11-19

PRIOR FILING DATE: 1997-11-19

PRIOR FILING DATE: 1997-11-19
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Mitchinson, C
APPLICANT: Wendt, Dan J.
TITLE OF INVENTION: NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local s
Matches 90
                                                                                                                                                                                                                                                         SEQ ID NO 21
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SEQ ID NO 5
LENGTH: 386
                                                                             Matches
                                                                                                                    Query Match
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TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                              FILE REFERENCE: GC555
CURRENT APPLICATION NUMBER: US/09/216,295
CURRENT FILING DATE: 1998-12-18
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TITLE OF INVENTION:
FILE REFERENCE: GC5
                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                       LENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 SVSELDLKAFIDDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 PRTNGVN-RTEIMIWFNRVGPVQPIGSPVGTAHVGGRSWEVWTGSNGSNDVISFLAPSAI 215
34
                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 ELCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGN-FTITRADHDNGNNVA--AYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 GAPKSYPSVYDGCHYGNCAPRTTLPMRISSIGSAPSSVSYRYTGNGVYNAAYDIWLDP-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 PPAQANQQICDRYGTTTIQ-DRYVVQNNRWGTSATQCINV---TGNGFEITQADGSVPTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 PEPEPTVELCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGN-FTITRADHDNGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
QICDRYGTTTIQ-DRYVVQNNRWGTSATQCINV---TGNGFEITQADGSVPTNGAPKSYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWSFDVKDFVDQAVSHGLATPDWYLTSIQAGFEPWEGGTGLAVNSFSSAV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSGNGYSGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTT
                                                                                                  Similarity
                                                                                                                                                                                                                                                                              FastSEQ for Windows Version 3.0
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VENTION: No. 6287839el Cellulase Producing Actinomycetes,
VENTION: Cellulase Produced Therefrom and Method of Producing Same
                                                                                                                                                                                                                                                                                                                                                                                                                  Mitchinson, Colin
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                          No. 6268328el Variant EGIII-Like Cellulase Compositions
                                                                                              27.48;
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                                                                         Score 396.5; DB 4;
Pred. No. 1.1e-31;
27; Mismatches 99;
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Pred. No. 5.8e-32;
28; Mismatches 104;
                                                                                                                Length 312;
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US-09-104-308-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FENGTH: 371 amino acids
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                                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/974,0 FILING DATE: 19-NOV-1997
ATTORNEY/AGENT INFORMATION: NAME: Stone, Christopher L. REGISTRATION NUMBER: 35,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENY AFFACTON NUMBER: US/09/104, 3
FILING DATE: 24-JUN-1998
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
08/974,042
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OTTOATTON NUMBER: US/09/104,308
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STREET: Palo Alto
CITY: Palo Alto
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NO TITLE OF INVENTION: CE NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Van Solingen, APPLICANT: Weyler, Walter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 KDFVDQAVSHGLATPDWYLTSIQAGFEPWEGGTGLAVNSFSSAV 251
                                                                              97 AIYFGCHWGACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYS 156
                                                                                                                  34 QICDRYGTTTIQ-DRYVVQNNRWGTSATQCINV---TGNGFEITQADGSVPTNGAPKSYP 89
                                                                                                                                                        40 ELCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGN-FTITRADHDNGNNVA--AYP 96
                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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SVYDGCHYGNCAPRTTLPMRISSIGSAPSSVSYRYTGNGVYNAAYDIWLDP-TPRTNGVN 148
GGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDL 216
                                          SYYDGCHYGNCAPRTTLPMRISSIGSAPSSYSYRYTGNGVYNAAYDIWLDP-TPRTNGVN 148
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                                                                                                                                                                                                89; Conservative
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Van Solingen, Piet
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                                                                                                                                                                                                                  27.48;
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                                                                                                                                                                                                ; Score 396.5; DB 4; pred. No. 1.4e-31; 27; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GC539
                                                                                                                                                                                                                                      Length
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US-09-216-295-22
; Sequence 22, Application US/09216295
; Patent No. 6268328
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; OTHER INFORMATION: thermovebaceous
US-09-321-981-1
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NUMBER OF SEQ ID NOS:
SOSTWARE: FastSEQ for
SEQ ID NO 1
LENGTH: 371
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Best Local S
Matches 89
                    CURRENT APPLICATION NUMBER: US/09/216,295
CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 381
                                                                                                                                                                                                                       GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: PCT/US99/11971
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 09/104,308
PRIOR APPLICATION NUMBER: 09/104,308
PRIOR APPLICATION NUMBER: 09/974,042
PRIOR APPLICATION NUMBER: 08/974,042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: No. 6287839el Cellulase Producing Actinomycetes,
TITLE OF INVENTION: Cellulase Produced Therefrom and Method of Producing
FILE REFERENCE: GC540-2
                                                                                                                                                        APPLICANT: Mitchinson, Colin APPLICANT: Wendt, Dan J. TITLE OF INVENTION: No. 6268
                                                                                                                                          FILE REFERENCE:
      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                         149
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                                                            FastSEQ for Windows Version 3.0
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                                                                                                                                                          No. 6268328el Variant EGIII-Like Cellulase Compositions
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APPLICANT: Outtrup, Helle
APPLICANT: Outtrup, Helle
APPLICANT: Jorgensen, Per Lina
APPLICANT: Bjornvad, Mads Eskelund
TITLE OF INVENTION: Alkaline xyloglucanase
FILE REFERENCE: 5206.200-US
CURRENT APPLICATION NUMBER: US/09/110,959A
CURRENT FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 0822/97
PRIOR FILING DATE: 1997-07-07
PRIOR FILING DATE: 1997-07-07
PRIOR APPLICATION NUMBER: 00054,039
PRIOR APPLICATION NUMBER: 60/054,039
PRIOR FILING DATE: 1997-07-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
LENGTH: 261
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 261
TYPE: PRT
ORGANISM: Bacillus licheniformis ATCC 14580
155
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231 NDWYLTSVQAGFEPWQNGAGLAVNSFSSTVE 261
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                                                                                                                                                                                                                                                                                                                17.7%; Score 255.5; DB 4 30.6%; Pred. No. 9.6e-18;
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                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                              ed. No. 9.66
Mismatches
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Query Match 23.7%; Score 343; DB.4; Length 381; Best Local Similarity 36.5%; Pred. No. 3.1e-26; Matches 77; Conservative 31; Mismatches 97; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 TDLPVRLDTVSAAPSSISYGFVDGAVYNASYDIWLDPTARTDG--VNQTEIMIWFNRVGP 170
                                                                                                                                                                                                                                                                                                                                     54 RYRVINNVWGAETA----OCIEVGLETGNFTITRADHD-----NGNNVAAYPAIYF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 GRYVVQNNRWGSTAPQCV-TATDTG-FRVTQADGSAPTNGAPKSYPSVFNGCHYTNCSPG 112
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                                   ELMIWLNWNGGVMPGGSRVATVELAGATWEVW--YAD----WDWNYIAYRRTTPTTSVSE 213
                                                                                                                                                                        GCHW-GACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNWNGG 170
EIMIWLN-NTNAGPAGSYVETVSIGGHSWKVYKGYIDAGGGKGWNVFSFIRTANTQS-AN
                                                                                                                                 GWHWTEGYTAGSGFPTRLSDQKNINTKVSYSISANGTYNAAYDIWLHNTNKASWDSAPTD 154
                                                                                                                                                                                                                                                                      KYYIFNNVWGADQVSGWWQTI------YHNSDSDMGWVWNWPSNTSTVKAYPSIVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
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LNIRDFTNYLADSKQWLSKTKYVSSVEFGTEVFGGTGQINISNWDVTVR 261

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RESULT 9
US-09-216-295-24
; Sequence 24, Application US/09216295
; Patent No. 6268328
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; Sequence 12, Application US/08032848C
; Patent No. 5475101
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                                                                                                                                                                                                                                                                                                                                                                  Query Match 17.6
Best Local Similarity 32.0
Matches 73; Conservative
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
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APPLICANT: Lorch, Jeffrey D.
TITLE OF INVENTION: Purification and
TITLE OF INVENTION: EG III Cellulase
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: HOID, MARGATER A.
REGISTRATION NUMBER: 33,401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,742-7356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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ADDRESSEE: Genencor International STREET: 180 Kimball Way CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                 186 NIRHFTDYLVQTKQWMSDEKYISSVEFGTEIFGGDGQIDITEWRVDVK
                                                                                                                                    215
                                                                                                                                                                       129
                                                                                                                                                                                                     163
                                                                                                                                                                                                                                                      104 WGA-CTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELM 162
                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                   16 KYYLFNNVWGKDEIKGWQQTIFYNSPISMG---WNWHWPSSTH----SVKAYPSLVSGWH 68
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TOPOLOGY: lir
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                      DLKAFIDDAV-ARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTVQ 261
                                                                                                                                                                                                                                                                                                                                   RYRVINNVWGAETAQ------CIEVGLETGNETITRADHDNGNNVAAYPAIYFGCH 103
                                                                                                                                                                                                   IWLN-WNGGVMPGGSRVATVELAGATWEV---WYADWD----WNYIAYRRTTPTTSVSEL 214
                                                                                                                                                                    IWLNDTNAG--PAGDYIETVFLGDSSWNVFKGWINNADNGGGWNVFSFVHTSGTNSAS-L 185
                                                                                                                                                                                                                                      WTAGYTENSGLPIQLSSNKSITSNVTYSIKATGTYNAAYDIWFHTTDKANWDSSPTDELM
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MAR 17 1993
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; SOFTWARE: FastSEQ for Windows V.; SEQ ID NO 5; LENGTH: 259; TYPE: PRT; ORGANISM: Aspergillus aculeatus US-09-216-295-5
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; SEQ ID NO 24
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Erwinia carotovara
US-09-216-295-24
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Patent No. 6268328
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Best Local Similarity
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CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
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CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
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APPLICANT: Wendt, Dan J.
TITLE OF INVENTION: NO.
FILE REFERENCE: GC555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
  125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 IWLN-WNGGVMPGGSRVATVELAGATWEVWYADW------DWNYIAYRRTTPTTSVSEL 214
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                                                                                                                              94 AYPAIYFGCHWGACTSNSGL---PRRVQELSDVRTSWTLTPITTG-RWNAAYDIWFSPVT 149
                                                                                                                                                                                                                  40 ELCGRWDARDVAGGRYRVINNVWGAET---AQCIEV--GLETGNFTITRADHDNG-NNVA 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 RYRVINNVWGAETAQ------CIEVGLETGNFTITRADHDNGNNVAAYPAIYFGCH 103
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                                        NSGNGYSGGAELMIWLNWNGGYMPGGSRVATVELAGATWEVWY-ADWDWNYIAYRTTPT 208
                                                                                                                                                                         QLCDQY--ATYTGGYYTINNNLWGKDAGSGSQCTTVNSASSAGTSWSTKWNWSGGENSVK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WTAGYTENSGLPIQLSSNKSITSNVTYSIKATGTYNAAYDIWFHTTDKANWDSSPTDELM 160
NHVT-WSGDYELMIWLARYGGVQPIGSQIATATVDGQTWELWYGANGSQKTYSFVAPTPI 183
                                                                                      SY-----ANSGLTFNKKLVSQISQIPTTARWSYDNTGIRADVAYDLFTAADI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IWLNDTNAG--PAGDYIETVFLGDSSWNV-FKGWINADNGGGWN-VSFVHTSGTNSAS-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version
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31.6%;
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                                                                                                                                                                                                                                                           36; Mismatches
                                                                                                                                                                                                                                                           Score 224.5; DB 4;
Pred. No. 1.2e-14;
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                                                                                                                                                                                                                                                                                                        Length 259;
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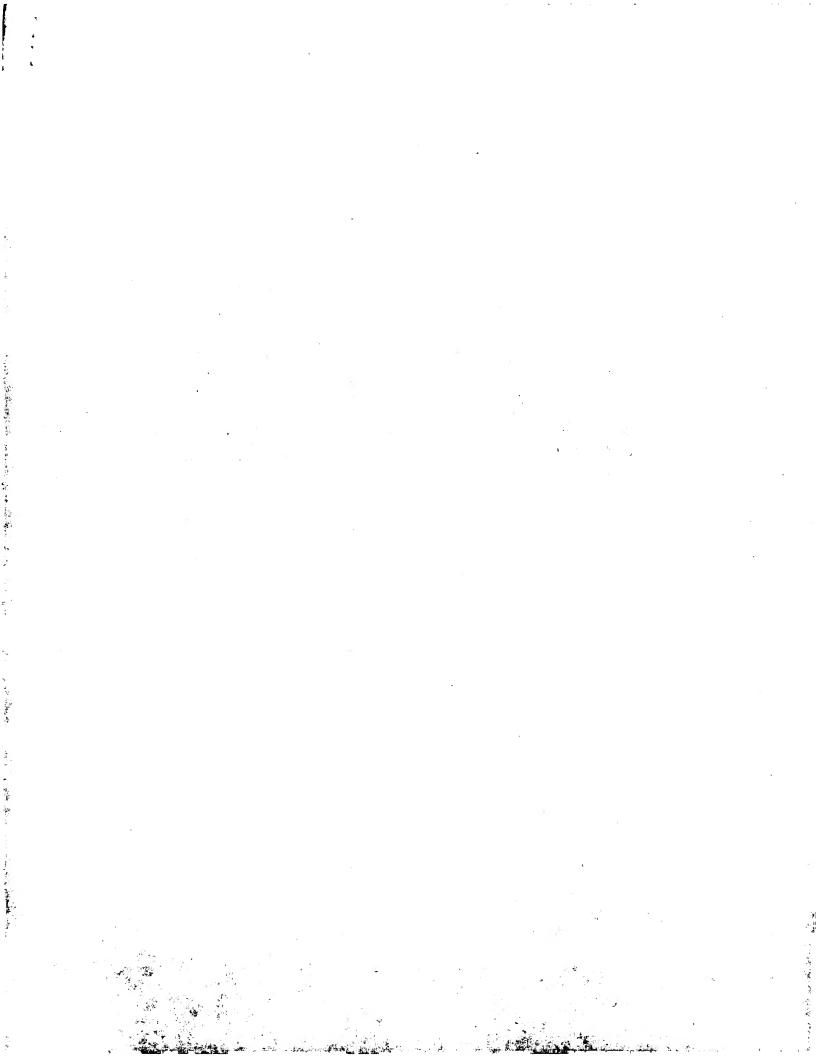
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SOFTWARE: FastSEQ for W
SEQ ID NO 7
LENGTH: 239
TYPE: PRT
ORGANISM: Aspergillus k
US-09-216-295-7
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US-09-216-295-7
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; ORGANISM: Humicola insolens US-09-216-295-10
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                                                      CURRENT APPLICATION NUMBER: US/09/216,295
CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 253
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09216295 Patent No. 6268328.
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Best Local Similarity 32.1%;
Matches 78; Conservative 3
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                                                                                                                                                                    APPLICANT: Mitchinson, Colin
APPLICANT: Wendt, Dan J.
TITLE OF INVENTION: NO. 6268328el Variant EGIII-Like Cellulase Compositions
FILE REFERENCE: GC555
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CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
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APPLICANT: Wendt, Dan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
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                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                       237 SVQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 TVQ 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 RRTTPTTSVSELDLKAFIDDAVA-RGYIRPEWYL--HAVETGFELWEGG-AGLRSADFSV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 PWQNGAGLAVNSFSSTV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 LWEGGAGLRSADFSVTV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 TSF-QGDVNDFFKYLTQNHGFPASSQYLITLQFGTEPFTGGPATLSVSNWSASVQQAGFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 AYPAIYFGCHWGACTSNSGL---PRRVQELSDV----RTSWTLTPITTGRWNAAYDIWFS 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVTNSGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY----ADWDWNYIAY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLCDQY--ATYTGGVYTINNILWGKDAGSGSQCTTVNSASSAGTSWSTKWNWSGGENSVK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SY-------ANSGLSFNKKLVSQISHIPTAARWSYDNTCIRRGR---AYDLFTA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 3.0
                                                                                                    FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 214; DB 4; L
Pred. No. 1.2e-13;
17; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 239;
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US-08-032-848C-13
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                                                    Query Match 14.7
Best Local Similarity 31.1
Matches 73; Conservative
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Best Local Similarity
Matches 73; Conserva
                                                                                                                                                                                                                                                                   TELEFAX: 415 742-7217
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 742-7356
TELEPHONE: 415 742-7217
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 4...
ATTORNEY/AGENT INFORMATION:
NAME: Horn, Margaret A.
NAME: Horn, Margaret 33,401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Purification and TITLE OF INVENTION: EG III Cellulase
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                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 YRRTTPTTSVSEL--DLKAFIDDAVA-RGYIRPEWYLHAVETGFELWEGG-AGLRSADF 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 DIWFSPVTNSGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWYADWDWNYIA 201
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: MAR 17 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 180 Kimball way
CITY: South San Francisco
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 EPEPTVELC---GRWDARDVAGGRYRVINNVWGAETA----QCIEV-GLETGNFTITRAD 85
                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVFTARDPDHPN-WGGDYELMIWLARYGGIYPIGTFHSQVNLAGRTWDLW-TGYNGNMRV 190
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180 Kimball Way
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Lorch, Jeffrey D.
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MAR 17 1993
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                                                      14.7%; Score 213; DB 1; Length 221; 31.1%; Pred. No. 1.3e-13; tive 40; Mismatches 92; Indels
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US-09-216-295-20
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SEQ ID NO 20
LENGTH: 246
TYPE: PRT
                                                                                                                                                            Sequence 9, Application US/09216295 Patent No. 6268328 GENERAL INFORMATION:
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APPLICANT: Witchinson, Colin
APPLICANT: Wendt, Dan J.
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Best Local Similarity
Matches 71; Conserv
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CURRENT APPLICATION NUMBER: US/09/216,295
CURRENT FILLING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                TITLE OF INVENTION: NO FILE REFERENCE: GC555
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CURRENT FILING DATE: 1998-12-18
NUMBER OF SEO ID NOS: 41
                                                                                                                   APPLICANT: Mitchinson, Colin APPLICANT: Wendt, Dan J.
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                                                                                                                                                                                                                                                                                                    233 DATLTVSSYSVSV 245
                                                                                                                                                                                                                                                                                                                                                                                    177
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                                                                                                                                                                                                                                                                                                                                           248 GAGLRSADFSVTV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VANVAYDLF----TSSSAGGDSEYEIMIWLAALGGAGPISSTGSSIATVTLGGVTWSLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 -- NAAYDIWFSPVTNSGNGYSGGAELMIWLNWNGGVMP---GGSRVATVELAGATWEVWY 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 SY------ANSGLTENKKLYSQISQIPTTARWSYDNTGIRADVAYDLETAADI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 AYPAIYFGCHWGACTSNSGL---PRRVQELSDVRTSWTLTPITTG-RWNAAYDIWFSPVT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 ----WHTTWSWSGGSSSVKSYANAAYQFTSTKLNSLSSIPTSW------KWQYSTTDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 DFCGQWDTATV--GNFIVYNNLWGQDNA---DSGSQTG-----VDSANGNSIS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 QLCDQY -- ATYTGGVYTINNNLWGKDAGSGSQCTTVNSASSAGTSWSTKWNWSGGENSVK
                                                                                                                                                                                                                                                                                                                                                                              GPNGSMQVYSEVA----SSTTESESADLMDFINYLAENQGLSSSQYLTHVQAGTEPFTGT
                                                                                                                                                                                                                                                                                                                                                                                                                 AD----WDWNYIAYRRTTPTTSVSELDLKAFIDDAVARGYIRPEWYLHAVETGFELWEG- 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGCHWGACTSNSG-------LPRRVQELSDVRTSWTLTPITTGRW-----
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for Windows Version 3.0
                                                                                                No. 6268328el Variant EGIII-Like Cellulase
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                                                                                                  Compositions
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; SEQ ID NO 9;
LENGTH: 253;
TYPE: PRT;
ORGANISM: Humicola grise1
US-09-216-295-9
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В
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Best Local Similarity 20...
Thes 70; Conservative
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242 ARFTCRDF
                             249 AGLRSADF
                                                                                                                                                     133 TTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY 192
                                                             182 TGYNGNMRVYSFLPPSGDIRDFSCDIKDFFNYLERNHGYPAREQNLIVYQVGTECFTGGP 241
                                                                                                                                                                                        75
                                                                                                                                                                                                                    28 EPRQIRSLCELYGYW-----SGNGYELLNNLWGKDTA------TSGWQCTYLDGTNNG 74
                                                                                                                                                                                                                                                                      34 EPEPTVELC---GRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGN 90
                                                                                       ADWDWNYIAYRRTTPTTSVSEL--DLKAFIDDAVA-RGYIRPEWYLHAVETGFELWEGG- 248
                                                                                                                                                                                    -----GIQWNTAWEWQGAPDNVKNYPYVGKQIQRGRKISDINSMRTSVSWTYDR- 123
249
                             256
                                                                                                                                                                                                                                                                                                                                14.6%;
28.2%;
                                                                                                                                                                                                                                                                                                               ; score 210.5; DB 4;
; pred. No. 2.8e-13;
31; Mismatches 96;
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Search completed: August 15, 2002, 10:52:08 Job time: 172 sec



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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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84.5
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probable peptidase
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dihydrodipicolinat
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                                                          arabinofuranosidas hypothetical prote hypothetical prote chitinase (EC 3.2.
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                hypothetical prote probable outer mem
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RESULT 1 JC2571 JC2101ase (EC 3.2.1.4) precursor - Streptomyces rochei (s N;Alternate names: endo-1,4-beta-glucanase; endoglucanase C.Species: Streptomyces rochei		.0	5.6	81.5 5	81.5 5.6	81.5 5.6	81.5 5.6	82 5.7	82.5 5.7	82.5 5.7	36 82.5 5.7 820	83 5.7	83 5.7	83	83 5.7	83 5.7	83 5	
sor		ν	N	_	ш	N	N	μ.	ب	N	N	N	N	N	N	N	N	
· - Streptomyces rochei (strain ·-glucanase; endoglucanase	ALIGNMENTS	T36249	G72658	VGIHE3	VGIHE2	AE3259	A47726	RLCSD	A43573	S59077	A40633	T29434	F75356	н64802	н85567	н90717	S06330	
ei (strain A2) anase		CDA peptide synthe	probable Vir B11 A	E2 glycoprotein pr	E2 glycoprotein pr	extracellular seri	dis1-suppressing p	ricin D precursor	E2 glycoprotein pr	cellulose 1,4-beta	chitinase (EC 3.2.	beta-galactosidase	serine/threonine p	ybfM protein - Esc	hypothetical prote	hypothetical prote	ricin E - castor b	

C; Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 22-Oct-1999 C; Accession: JC2571; S34392 C; Recession: JC2571; S34392 R; Perito; B: Hanhart; E-; Irdani; T; Tqbal, M.; McCarthy, A.J.; Mastromei, G. Gene 148, 119-124, 1994 A; Title: Characterization and sequence analysis of a Streptomyces rochei A2 endogluca A; Reference number: JC2571; MUID:95011642 A; Accession: JC2571 A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as A;Pathway: cellulose degradation C;Superfamily: bacterial cellulose-binding domain homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;1-37/Domain: signal sequence #status predicted <SIG>F;1-37/Domain: endoglucanase #status predicted <ANT>F;279-380/Domain: bacterial cellulose-binding domain homology <BCB> A; Gene: eglS C; Function: A;Molecule type: DNA A;Restidues: 1-382 <PER> A;Restidues: 1-382 <PER> A;Cross-references: EMBL:X73953; NID:g393391; PIDN:CAA52139.1; PID:g393392 A;Cross-references: EMBL:X73953; NID:g393391; PIDN:CAA52139.1; PID:g393392 A;Note: this cellulolytic strain was isolated from the gut of termites

F;280-379/Disulfide bonds: #status predicted

Qy 밁 Qy γQ В В Q Query Match 24.3%; Best Local Similarity 36.2%; Matches 77; Conservative 168 107 108 TSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWINW 167 225 LAGNDWYLTSIQAGFEPWQNGAGLAVNSFSSTV 257 49 50 VAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVA--AYPAIYFGCHWGAC 107 YIRPEWYLHAVETGFELWEGGAGLRSADFSVTV 260 VGQIQPIGSQVGTASVAGRTWEVWSGGNGTNDVLSFVAPSAMSSWSFDVMDFVRATVARG NGGVMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDLKAFIDDAVARG VIQGRYVVQNNRWGTSATQCV-TATDSG-FRVTQADGSVPTNGAPKSYPSVFNGCHYTNC 106 32; Score 352; DB 2 Pred. No. 1e-21; Mismatches DB 2; 98; Indels Length 382 6. Gaps 227 224

prot

RESULT JU0328

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A; Cross-references: EMBL:X52525; NID:g2287; PIDN:CAA36757.1; PID:g2288
A; Cross-references: EMBL:X52525; NID:g2287; PIDN:CAA36757.1; PID:g2288
A; Marso, A.; Okada, H.; Hara, S.; Ikenaka, T.; Murao, S.; Arai, M.
Curr. Genet. 18, 217-222, 1990
A; Tittle: Cloning and sequence analysis of a cDNA for cellulase (FI-CMCase) from A; Reference number: S14118; MUID:91064758
A; Reference number: S14118
A; Accession: S14118
A; Residues: 1-237 < COI2>
A; Cross-references: EMBL:X52525; NID:g2287; PIDN:CAA36757.1; PID:g2288
A; Accession: S40186
A; Accession: S40186
A; Residues: 17-18;42-49,'X',51-54,'X';66-79;90-111;136-205,'XX',208-211 < COI3>
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
S12610
Cellulase (EC 3.2.1.4) precursor - Aspergillus aculeatus
C:Slate: Or-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jul-2000
C:Accession: S12610; S14118; S40186; J00458.
C:Accession: S12610; Okada, H.; Murao, S.; Kawaguchi, T.; Arai, M.
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C:Function:
A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in A;Pathway: cellulose degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
C;Keywords: signal sequence #status predicted <SIG>F;33-264/Product: cellulase #status experimental <MAT>
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R.Saarilahti, H.T.; Henrissat, B.; Palva, E.T.
Gene 90, 9-14, 1990
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A;Cross-references: GB.M32399; NID:g148389; PIDN:AAA24817.1; PID:g148390
A;Experimental source: strain SCC3133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: part of this sequence, including the amino end C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTALLE: Cels: a novel-endoglucanase identified from Erwinia carotovora subsp. carotovora, Reference number: JU0328; MUID:90337352
A; Accession: JU0328
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N;Alternate names: endo-1.4-beta-glucanase; endoglucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIRHFTDYLVQTKQWMSDEKYISSVEFGTEIFGGDGQIDITEWRVDVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLKAFIDDAV-ARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTVQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IWLN-WNGGVMPGGSRVATVELAGATWEVWYADW------DWNYIAYRRTTPTTSVSEL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WTAGYTENSGLPIQLSSNKSITSNVTYSIKATGTYNAAYDIWFHTTDKANWDSSPTDELM 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYYLENNVWGKDEIKGWQQTIFYNSPISMG---WNWHWPSSTH----SVKAYPSLVSGWH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IWLNDTNAG--PAGDYIETVFLGDSSWNV-FKGWINADNGGGWNVFSFVHTSGTNSAS-L 216
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Pred. No. 1.2e-13;
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C:Date: 11-Jun-1999 #sequence_revision
C:Accession: A72241
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE001800; GB:AE000512; NID:g4982090; PIDN:AAD36592.1; PID:g498
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-274 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316 A;Accession: A72241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 399,
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Best Local (
           198
                                  199. YIAYRRTTPTTSVS-ELDLKAFIDDA---VARGYIRPEWYLHAVETGFELWEGGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                         86
                                                                                                                                                                               98 IYFGCH-WGACTSNSG---LPRRVQELSD--VRTSWTL----TPITTGRWNAAYDIWFS 146
                                                                                                                                                                                                                               38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
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YLAFRLTTPMKEGKVKINVKDFVQKAAEVVKKHSTRID---NFEELYFCVWEIGTEFGDP 254
                                                                                            PVTNSGNGYSGGAELMIWLNWNGGVMPGGSRV----ATVELAG:----ATWEVWYADWDWN 198
                                                                       RSPDQTSVSSGDAEIMVWF-YNNVLMPGGQKVDEFTTTVEINGVKQETKWDVYFAPWGWD
                                                                                                                                               IYYGYKPWAG---HNSGVEFLPVKVKDLPDFYVTLDYSIWYENNLPI-----NLAMETWIT
                                                                                                                                                                                                                   TMEL-NEWNVKSYEG-----ETWLKEDGEKVEFYADLYNIVLQNPD----SWVHGYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSF-QGDVNDFFKYLTQNHGFPASSQYLITLQFGTEPFTGGPATLSVSNWSASVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSVSELDLKAFIDDAVA-RGYIRPEWYLHAVETGFELWEGG-AGLRSADFSVTVQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSGNGYSGGAELMIWLNWNGGYMPGGSRVATVELAGATWEVWY-ADWDWNYIAYRRTTPT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SY------ANSCLTFNKKLVSQISQIPTTARWSYDNTGIRADVAYDLFTAADI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLCDQY--ATYTGGYYTINNNLWGKDAGSGSQCTTVNSASSAGTSWSTKWNWSGGENSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NHVT-WSGDYELMIWLARYGGVQPIGSQIATATVDGQTWELWYGANGSQKTYSFVAPTPI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323-329, 1999
                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clayton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.A.; Gill, s
A.M.; Cotton,
                                                                                                                                                                                                                                                                                                                14.0%; 28.3%;
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31.1%;
                                                                                                                                                                                                                                                                                                 40;
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                                                                                                                                                                                                                                                                                             Score 202; DB 2
Pred. No. 2e-09;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 213; DB 2;
Pred. No. 2.1e-10;
0; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-Jun-1999
                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                               87;
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                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from genome
                                                                                                                                                                                                                                                                                           16;
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C;Species: Aspergillus niger
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
C;Accession: S5931; $60657; J80730
R;Sakamoto, S.; Tamura, G.; Ito, K.; Ishikawa, T.; Iwano, K.; Ni
Curr Genet. 27, 435-439, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:99295987
A;Accession: H70895
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                      A;Pathway: cellulose degradation
C;Keywords: blocked amino end; glycosidase; hydrolase; polysaccharide
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-239/Product: cellulase #status predicted <MAT>
                                                                                                                                                 C; Function:
                                                                                                                                                                A;Cross-references: EMBL:D12901; NID
A;Note: the source is designated as
A;Accession: S60657
A;Molecule type: protein
A;Residues: 76-86;176-186 <SAK2>
A;Note: the source is designated as
                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-239 < SAK>
                                                                                                                                                                                                                                                                                                                                    A; Reference number: S55931; MUID:96059347 A; Accession: S55931
                                                                                                                                                                                                                                                                                                                                                                           Curr. Genet. 27, 435-439, 1995
A;Title: Cloning and sequencing of cellulase cDNA from Aspergillus kawachii and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cellulase (EC 3.2.1.4) precursor - Aspergillus niger N;Alternate names: carboxymethylcellulase I; endo-1,4-beta-glucanase C;Species: Aspergillus niger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-151 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: H70895
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C;Date: 17-Jul-1998 *sequence_revision 17-Jul-1998 *text_change
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                                                                                                                         A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGVMPGGSRVATVELAGATWEVWYADWDW-NYIAYRRTTPTTSVSELDLKAFIDDAVARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNLPTEVGQILSAPTSIDYNYPTTGVWDASYDICLDSTPKTTGVN----QQEIMIWFNHQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTTAAKFGWTFRDFSVEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
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                                                                                                                                                                                                                                                   NID:g217812; PID:g217813 as Aspergillus kawachii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 194; DB 2; Pred. No. 4.7e-09;
                                                                                                                                                                  Aspergillus
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                                                                                                                                                                    kawachii
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                                                                                                                                                                                                                                                                                                                                                                                                                   Iwano, K.; Nishiya, N
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A;Reference number: A72200; MUID:99287316
A;Recession: H72240
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <ARN>
A;Cross-references: GB:AE001800; GB:AE000512; NID:g4982090; PIDN:AAD36591.1; PID:g498
C;Genetics:
A;Gene: TM1524
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H72240
endoglucanase - Thermotoga maritima (strain MSB8)
c;Species: Thermotoga maritima
c;Species: Thermotoga maritima
c;Species: 11-Jun-1999 #text_change 21-Jul-2000
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt,
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240
                                                                     253
                                                                                                                                               182 LAFRLKDPVKKGRVKFDVRHFLDAAGKALSSSARVKDFEDLYFTVWEIGTEF--GSPETK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 VAAYPAIYFGCH-WGACTS-NSGLPRRVQELS--DVRTSWTLTPITTGRWNAAYDIWFSP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                     SADF
                                                                                                                                                                                                                                                                                                                                         VTNSGNGYSGGAELMIWLNWNGGVMPGGSR------VATVELAGATWEVWYADWDWNY 199
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SAQF
                                                                                                                                                                                                                         IAYRRTTPTTSVS-ELDLKAFIDDA-----VARGYIRPEWYLHAVETGFELWEGGAGLR
                                                                                                                                                                                                                                                                                               EKYQTEASIGDVEIMVWFYFN-NLTPGGEKIEEFTIPFVLNGESVEGTWELWLAEWGWDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLGYPEFYYGYKPWENHTAEGSKLPVPVSSMKSFSVEVSFDIHHEPSLPLNFAMETWLTR
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Pred. No. 2.
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Pred. No. 2.1e-05;
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submitted to GenBank, April 2001
A; Description: Sulfolobus solfatar
A; Reference number: A99139
A; Accession: G90291
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-332 <KUR>
A; Cross-references: GB:AE006641; N
C; Genetics:
A; Gene: SS01354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endoglucanase precursor [imported] - Sulfolobus solfataricus (;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001. #text_change 24-May-2001 C;Accession: 690360 R;She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redd arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001 A;Description: Sulfolobus solfataricus complete genome.
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C;Genetics:
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A; Accession: G90360
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                                                                                                                                                                               NVWGAETAQCIEVGLETGNFT----ITRA------DHDNGNNVAAYPAIYFG 101
PGN---GDIEIMVWL-FSQNLQPAGQQVGEVVIPIYINHTLVNATFQVWKMKNVPWGGWE
                                    SGNGYSGGAELMIWLNWNGGYMPGGSRVATV-----ELAGATWEVW----YADW-DWN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGNGYSGGAELMIWLNWNGGVMPGGSRVATV-----ELAGATWEVW---YADW-DWN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WNAKNYNGNYTMVFNPL----ARTLSV-----SFNLTQVKPLEWTNG-----YPEIYVG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRA----DHDNGNNVAAYPAIYFG 101
                                                                           RKPWDTSYAGNIFPMRIGNMTPFMVSFYINLTKLDPSINFDIASDAWIVRPQIAFSPGTA 206
                                                                                                                  CH-WGACTSNSGLPRRVQELSDVRTSWTLT------PITTGRWNAAYDIWFSPVTN 150
                                                                                                                                                        NMWNAKT-----WNGNYTMVFNPLTRTLSVSFNLTQVNPLQWTNG-----YPEIYVG 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CH-WGACTSNSGLPRRVQELSDVRTSWTLT-----PITTGRWNAAYDIWFSPVTN 150
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                                                                                                                                                                                                                                  9.6%; Score 139; DB 2;
24.7%; Pred. No. 0.00041
tive 26; Mismatches 6
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probable peptidase - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: B70528
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go
R:Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete
A;Reference number: A70500; MUID:98295987
A,Accession: B70528
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
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A;Accession: H82261
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A; Residues: 1-957 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.J; Bass, S.; Qin, I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: H82261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 FPDGDNGKEPEPEPTVELCGRWDARDVA--GGRYRVINNVWGAETAQCIEVGLETGNF
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                                                                                                                                                                                                                                                                                                                                                                                          AVDMY - - - NSKGERVWSVANDDTGSGKIGVSAYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVNVKDIKAIDLTW-----GKYYWGGYHLLA-LDFRMSNGSVISMGSKNYAYSKQTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FATGDNARFAVLEHDGTI----KWEINNTANPGGGVQAVSNFLGKAQA-----VETSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --MPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDLKAFIDDAVARGYI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKVYGYQPNNNPASIALAVD-----GKISVRSGF--AIDAIG--ASASTLVGGTGGNLNA 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITRADHDNGNNVAAYPAIYFGCHWGACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYDI------WFSPVTNSGNGYSGGAELMIWLNW---NGGV-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -KAWTAGWLLDGVQFELAT-QNGTNDLDVKGI----VYAGYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 99; DB:
Pred. No. 2.7;
37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                            690
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H.; Dragoi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Dodson, R. I.; Sellers
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Holroyd,
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263

VPIGYILKNMGSYIEKAGVNIYNVNTYYLDAIQVGME

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redd arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-673 <COL>
                                                                                                                                       밁
                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein celB [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: H90425
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H90425
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-322 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A99139
A;Accession: H90425
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Best Local S
Matches 59
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Best Local Similarity
Matches 44; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    488
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                     213
                                                                                                     170
                                                                                                                                                                  112 GLPRRVQELSDVRT--SWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNWNG 169
                                                             203
                                                                                                                                           143 SLPMIVLRLPNFYSILNYSVYLINGSIDDFSYDIWLSQNPNITSLQYGDFEIMIWMYWNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 6.7%; Score 97; DB 2; Length 673 Local Similarity 22.7%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 EPEPEPTVE-LCGR-WDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNG
                                                                                                                                                                                                                           83 IGYALGNVNMTININYLHVAINLSQISKISSNVVDGYPGLMYGQELWWPFMYRTTQLQFL 142
                                                                                                                                                                                                                                                               72 VGLETGNFTIT------RADHDNGNNVAAYPAIYFG--CHWGACTSNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSRTPTYDGVLGRLWLAR---GGTYALANIRGGGE-----
                                                                                                   G-----DWDWNYIAYRRTTPTTSVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEYGDPDNPDDWKFISEYSPYQNISANRKYPPVLMTTSTR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSGNGYSGGAELMIWLNWNGGVMPG------GSRVATVE------LAGATWE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----YGPGWHTQAMREGRDKVAQDFAAVATDLVTRGITTA----
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                                                             NLSHTPYFIYVGNMSIPTLINGKIENLSWEVYVLPRTGSANGWTGVYFLSPLKEPKAEFG
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-LDLKAFIDDAVARGYIRPEWYLHAVETGFE ::::|: | :| | :| | |:: | |
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PEWYLHAVETG
                                                                                                                                                                                                                                                                                                       6.6%; Score 95.5; Di
20.3%; Pred. No. 1.6;
tive 33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                 DB
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                                                                                                                                                                                                                                                                                                           95;
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                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                         45;
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                                                             262
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hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72204
                                                                                                                                                                                                                                                            C;Accession: B84221
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Las; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483
A;Accession: B84221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
B84221
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A;Title: Evidence for lateral gene transfer A;Reference number: A72200; MUID:99287316
A;Accession: D72204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garrett, M.M.; Stewart, A.M.; Cotton,
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A; Residues: 1-443 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Vng0631c [imported] - Halobacterium sp. NRC-1C; Species: Halobacterium sp. NRC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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                                                                                                                         A; Gene: VNG0631C
                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-604 <S
                                                                                                                                                                                                                                     A; Status: preliminary
Query Match
Best Local S
Matches 59
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 A-----WGRKISFGADYAVDYEI-----YFWWAGGSGLDSNNFCEWNGLDWNY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMIWLNWNGGVMPGGSRVATVELAGATWEVWYA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCHWGACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGRYRVINNVWGAE--TAQCIEVGLETGNF----TITRADHDNGNNV----AAYPAIYF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --YIGFDTQNS-
    Similarity
59; Conser
                                                                                                                                                                                         1-604 <STO>
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Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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23.2%; Pred. No.
                      6.4%; Score 93; I
23.3%; Pred. No. 5.
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EPTVELCGRWDARDVAGG 53

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Search completed: August 15, 2002, 10:51:39 Job time: 178 sec
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A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343
A;Accession: G69514
A;Accession: G69514
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-741 (KLE)
A;Residues: 1-741 (KLE)
A;Cross-references: GB:AE000958; GB:AE000782; NID:g2689281; PIDN:AAB89151.1; PID:g264842
C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF2119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein AF2119 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec:1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
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                                                                                                          372 YGNFDDADWDGACIAVGSTTP 392
                                                                                                                                                                                     320 VRVNWYVDENSVLKPYPIPVVOKFTGNR-----
                                                                                                                                                                                                                    163 IWLNW----NGGVMP------GGSRVATVELAGATWEVWY------- 192
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                                                                                                                                                                                                                                                           261 LSDKLRVNFVAKIEDVMINCNAYTITINRAILAENVAITÞGSYDITLVGRMYYSGGAD-W 319
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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163.5
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Gapop 10.0 , Gapext 0.5
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YL1_ACCSK
YL1_BOVIN
GUB_RHOMR
CL2_CVPPR
CHIT_STRPL
VGL2_CVPPI
GURB_CCLFI
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6 porcine tra
2 streptococc
4 mycobacteri
7 homo sapien
5 escherichia
3 alteromonas
9 clostridium
3 bacilus su
5 magnaporthe
9 sulfolobus
6 caprine art
7 porcine tra
9 schizosacch
                                                                                                                                                                                                                                 3 streptomyce
9 cellulomona
9 porcine tra
9 ricinus com
5 pasteurella
1 corynebacte
6 schizosacch
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104 WGA-CTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAVDIWF	WQQTIFYNSPISMG	IEVGLET(atch 17.5%; Score 252 cal Similarity 31.6%; Pred. No. 72; Conservative 39; Mismat	GNAL 1 32 HAIN 33 264 ENDOGLUCANASE S EQUENCE 264 AA; 29757 MW; E6D61388950C7	cobon; pp004316; Glyco.hydro.12; 1. sllulose degradation; Hydrolase; Glycosidas	IR; JU0328; JU0328. smr Pro; IPR002594; Glyco_hydro_12.	send an email to license@isb-sib.ch).	of by non-profit institutions as long additied and this statement is not removed. Intities requires a license agreement (See h	stween to entry is copyright. It is protected the Swiss Institute of Bioinformatic Pherical Swiss Institute. There were a considered the swiss of the swisses of the swisse	- SIMILARITY: BELONGS TO CELLULASE FAMILY HYDROLASES).	- CATALYTIC ACTIVITY: Endohydrolysis of 1, linkages in cellulose.	DelS: a novel endoglucanase identified from the carotovora.";	TRAIN-SCC3193; DDLINE-90337352; PubMed-2379837;	QUENCE FROM N.A., AND PARTIAL SEQUENCE.	 EFWINIA CAROCOVOTA. Bacteria; Proteobacteria; gamma subdivision; Enterobacteribacterium. NCBI_TaxID=554; 	STS.	sequence update) annotation update EC 3.2.1.4) (Endo	Rel. 15, Created)	1 WCA INS_ERWCA STANDARD; PRT; 264 AA.	ALIGNMENTS	77 5.3 2044 1 SIFZ_DROME 76.5 5.3 216 1 SPHB_IPOBA 76.5 5.3 270 1 KITM_MOUSE 76.5 5.3 318 1 ALYS_STRPN 76.5 5.3 327 1 A85B_MYCLE	5 5.4 877 1 5 5.4 1356 1 7 5.3 572 1 7 5.3 1481 1	8 5.4 852 1 5 5.4 722 1 5 5.4 846 1
/DIWFSPVTNSGNGYSGGAELM 162	PSSTHSVKAYPSLVSGWH 100	DNGN	DB 1; Length 264; 14; 86; Indels 31; Gaps 10;	3. 77AA CRC64;	se; Signal.			and for isb-sib.cl	counter through a contamoration - ics and the EMBL outstation - re are no restrictions on its	12 OF GLY	,4-beta-D-glucosidic	n Erwinia carotovora			Enterobacteriaceae;))-1,4-beta-glucanase S)				p91620 drosophila p10965 ipomoca bat Q97088 mus musculu p06653 streptococc p31951 mycobacteri	t a po	P03361 bovine leuk P16395 drosophila P06875 escherichia

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RESULT COMPASSAC ID GUN_ASPAC P2266 DT 01-AU DT 01-AU DT 15-DE Endog DE (Cell OS Asper OC Eukar OC Eukar OC Eukar OC Eurot OX NCBI_RA SEQUE RC STRAI RX MEDLI RA OO1 T RA GOOL TICC OT SEQUE RC STRAI RX MEDLI RX MEDLI RX MEDLI RX MEDLI RX MEDLI RX MEDLI RA OO1 T RA GOOL TICC OT SEQUE RC CO -1- SEQUE RC CO -1- SECC OT S
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                                                                             InterPro; IPR002594; Glyco_hydro_12.

Pfam; PF01670; Glyco_hydro_12; 1.

ProDom; PD004316; Glyco_hydro_12; 1.

Cellulose degradation; Hydrolase; Glycosidase; Glycosidase; Glycosidase; Glycosidase; Glycosidase; SIGNAL 1 16
                                                                                                                                                                                                                          EMBL; D00546; BAA00435.1; -. EMBL; X52525; CAA36757.1; -. PIR; J00458; J00458; J0458; J0458; J0458; J0458; S12610; S12610. PIR; S14118. S14118.
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Ooi T., Shinmyo A., Okada H., Murao S.,
"Complete nucleotide sequence of a gene
aculeatus cellulase (FI-CMCase).";
Nucleic Acids Res. 18:5884-5884(1990).
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01-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Endoglucanase I precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
(Cellulase) (FI-CMCASE).
Aspergillus aculeatus.
Eukaryota; Fuggi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergill
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P22669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Secreted.
INDUCTION: BY CELLULOSIC MATERIALS
MISCELLANEOUS: WILL ALSO HYDROLYSE
ALSO CONTAINING 1,3-LINKAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO CELLULASE FAMILY H (FAMILY 12 OF
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CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IWLN-WNGGVMPGGSRVATVELAGATWEVWYADW------DWNYIAYRRTTPTTSVSEL
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                A;
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                25560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okada H.,
             ¥.
ENDOGLUCANASE I.
PYRROLIDONE CARBOXYLIC AC
### BF173571A8AE6931 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S., Ikenaka
                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
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1,4-LINKAGES IN BETA-D-GLUCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawaguchi T., Arai M.; coding for Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $
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                                                                                                           Signal
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                                                   Query Match
Best Local S
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Best Local :
                                                                                               Pram; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
Cellulose degradation; Hydrolase; Glycosidase; SIGNAL 1 16
CHAIN 17 239 ENDOGLUCANASE A.
SEQUENCE 239 AA; 25769 MW; 16B0304A138276D(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GUNA_ASPAK
Q12679;
01-NOV-1997
                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                              EMBL; D12901;
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96059347; PubMed=7586029;
                                                                                                                                                                                   [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiom
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-IFO 4308
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus awamori (var. kawachi)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endoglucanase
clidogludanase A precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase
(Cellulase A) (Carboxymethylcellulase) (CMCase-I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 ELCGRWDARDVAGGRYRVINNVWGAET----AQCIEV--GLETGNFTITRADHDNG-NNVA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                          linkages in cellulose.
SIMILARITY: BELONGS TO CELLULASE FAMILY H (FAMILY 12 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                      HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSF-QGDVNDFFKYLTQNHGFPASSQYLITLQFGTEPFTGGPATLSVSNWSASVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSVSELDLKAFIDDAVA-RGYIRPEWYLHAVETGFELWEGG-AGLRSADFSVTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NHVT-WSGDYELMIWLARYGGYQPIGSQIATATVDGQTWELWYGANGSQKTYSFVAPTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY-ADWDWNYIAYRRTTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYPAIYFGCHWGACTSNSGL---PRRVQELSDVRTSWTLTPITTG-RWNAAYDIWFSPVT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLCDQY--ATYTGGYYTINNNLWGKDAGSGSQCTTVNSASSAGTSWSTKWNWSGGENSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SY---
                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                IPR002594;
                                         Conservative
                                                                                                                                                                                           BAA02297.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 35, Created)
1. 35, Last sequence update)
1. 35, Last annotation update)
Precursor (EC 3.2.1.4) (Endo-
                                                 11.3%;
27.3%;
                                                                                                                                                                             Glyco_hydro_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.78;
31.18;
                                         38;
                                                  Score 163.5; DB Pred. No. 4.9e-07
                                                                                                 ENDOGLUCANASE A.
; 16B0304A138276D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Ishikawa T., Iwano K.,
ulase cDNA from Aspergi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           cerevisiae.";
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                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                  There are no restrictions ng as its content is in
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                                                              DB 1;
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                                                                                                                                                                                                                                                                                                                                                   ACTIVITY.
1,4-beta-D-glucosidic
                                      97;
                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92;
                                                                                                                                       Signal.
                                                                                                                                                                                                                                                                                                                                                                                                    wano K., Nishiya
Aspergillus kawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 237;
                                      Indels
                                                            Length
                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus.
                                                                                                                                                                                                                                                                              EMBL
                                     33;
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                                                                                                                                                                                                                                                                             collaboration
                                                                                                                                                                                                                                                                           outstation
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                                    Gaps
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                                    11;
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                                                                                                                                 Query Match
Best Local :
                                                                                                                  Matches
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15-DEC-1998
15-DEC-1998
16-OCT-2001
                                                                                                                                                                                               Hydrolase; (ACT_SITE ACT_SITE SEQUENCE
                                                                                                                                                                                                                                                                                                          Pfam; PF00703; Glyco_hydro_2; 1.
Pfam; PF02836; Glyco_hydro_2_C; 1.
Pfam; PF02837; Glyco_hydro_2_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Obst M., Meding E.R., Vogel R.F., Hammes W.P.;
"Two genes encoding the beta-galactosidase of Lactobacillus sake.";
"Independent of the beta-galactosidase of Lactobacillus sake.";
"Independent of the beta-galactosidas of terminal, non-reducing beta-D-galactose residues in beta-D-galactosides.

Independent of the beta-D-galactosides.

SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.

SUBUNIT: SINILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROCLASES.
                                                                                                                                                                                                                                                                                                                                                          EMBL; X82287; CAA57730.1; -.
HSSP; P00722; 1BGL.
InterPro; IPR001649; Glyco_hydro_2.
                                                                                                                                                                                                                                                                                                                                                                                                                               entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-DSM 20017;
MEDLINE-96118231; PubMed-8574399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LACSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-galactosidase large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BGAL_LACSK
                                                                                                                                                                                                                                                              PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2;
                                                                                                                                                                                                                                                                                                PRINTS; PR00132; GLHYDRLASE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LACL
106 ACTSNSGLPRRVQELSDVRTSWILTPITTGRWN--AAYDIWESPVTNSG----NGYSGGA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lactobacillus sakei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95
                                                                      53 GRYRVINNV----WGAETAQCIEVGLETGNFTITRADHDNGNNVAAYP---AIYFGCHWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY-----ADWDWNYIAYRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPAIYFGCHWGACTSNSGL---PRRVQELSDVRTSWTLTPITTG-RWNAAYDIWFSPVTN 150
                                               GKRLVINGVNRHEWHPETGRTITAEDEAWDIACMQRNHINAVRTSHYPDRLSFYNGC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPINSWSG-DIKDFFNYLTQNQGFPASSQHLITLQCGTEPFTGGPATFTVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y-----SNSGLTFDKKLVSDVSSIPTSVTWSQDDTNVQADVSYDL-FTAANA 122
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                                                                                                                44;
                                                                                                                              Similarity
                                                                                                                                                                                                533
625 A
                                                                                                                                                                                                                                 Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
osidase large subunit (EC 3.2.1.23) (Lactase).
                                                                                                                  Conservative
                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                              6.48;
17.98;
                                                                                                                                                                                                533
72457 MW;
                                                                                                                  39;
                                                                                                                                 Score 93;
Pred. No.
                                                                                                                                                                                               NUCLEOPHILE (BY SIMILARITY). C658A3C46136B886 CRC64;
                                                                                                                                                                                                                              PROTON DONOR (BY SIMILARITY).
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                                                                                                                  Mismatches
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                                                                                                                                             DB 1;
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                                                                                                                  87;
                                                                                                                                               Length 625;
                                                                                                                Indels
                                                                                                                76;
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                                                                                                               Gaps
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RESULT
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Best Local
                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Richardson D.L., Quackenbush J.-Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artlach P., Kalne B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARCFU
                                                                                                                                                                                        Hypothetical protein; SIGNAL 1 22
CHAIN 23 741
SEQUENCE 741 AA; 820
                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a clotween the Swiss institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                       EMBL; AE000958; AAB89151.1; -. TIGR; AF2119; -.
                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98049343; PubMed=9389475
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                                                                              75
                                              DTDTITLYAKVVSNGNPVPDYPVKFYAEFDSQRIFLG---GAWTNSSGIAKLSFIPKNVG
                                                                             ETGNFTITRADHDNGNNVAAYPA-----IYFGCHWGACTSNSG-----LPRR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEYKATISDVESRMYATPAEIKAYLDNAPQKPFILCE-YMHDMGNSLGGMQSYIDLLSQY
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                                                                                                            l Similarity
49; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein AF2119 precursor
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-VQELSDVRTSWTLTPITTGRWNAAYDIWFSP----VTNSGN-GYSGGAELM 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                         741
82084 MW;
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                                                                                                                          6.48;
                                                                                                                                                                                                                                       Signal; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SLGNESYAGSVLEKMNA-----YYKQQDPTRLVHYEGVFRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaeoglobales; Archaeoglobaceae;
                                                                                                              21;
                                                                                                                           Score 93;
Pred. No.
                                                                                                                                                                                           HYPOTHETICAL PROTEIN AF2119; E8C7543552231583 CRC64;
                                                                                                                                                                                                                           POTENTIAL.
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                                                                                                              Mismatches
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                                                                                                                                            DB 1;
                                                                                                              51;
                                                                                                                                         Length 741;
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                                                                                                                                                                                                                                                                                                                                                                    restrictions
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MBL outstation -
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Best Local S
Matches 45
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01-AUG-1990
16-OCT-2001
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                           PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
Xylan degradation; Hydrolase; Glycosidase; Signal.
                                                                                                                                                                                                            Pfam; PF00457; Glyco_hydro_11; PRINTS; PR00911; GLHYDRLASE11.
                                                                                                                                                                                                                        InterPro; IPR001137; Glyco_hydro_11.
Pfam: PF00457; Glyco_hydro_11; 1.
                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium saccharobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                               PIR; S12745; S12745.
HSSP; P36217; 1XYO.
                                                                                                                                                                                                                                                                      EMBL; M31726; AAA23287.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endo-1,4-beta-xylanase precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-169679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XYNA_CLOSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372
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                50
                                    55
                                                                                                                                                                                                                                                                                                                                                                                                                                 linkages in xylans.
PATHWAY: XYLAN DEGRADATION.
                                                                                                                                                                                                                                                                                                                                                                                     C.acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                               CAUTION: Was originally thought to originate
                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO CELLULASE FAMILY G
                                                                                                                                                                                                                                                                                                                                                                                                           HYDROLASES).
               YSAFNTQAAPKTITSNEIGVNGGYDYELWK---DYGNTSMTLKNGGA----FSCQW---
                                    YRVINNVWGAETAQCIEVGLETG-NFTITRADHDNGN-----NVAAYPAIYFGCHWGAC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSDKLRVNFVAKIEDVMTNCNAYTTTNRAILAENVAITPGSYDITLVGRMYYSGGAD-W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IWLNW----NGGVMP------GGSRVATVELAGATWEVWY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ADWDWNYIAYRRTTP
                                                             45; Conserv
                                                                                                                   29
152
242
261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 40, Last annotation updat
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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261
152
242
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                                                           Score 88.5; D
Pred. No. 1.3;
28; Mismatches
                                                                                                                   ENDO-1, 4-BETA-XYLANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
; 339C3616F6FD14AE CRC64;
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                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              group;
                                                           ; 89
                                                                                                                                                                                                                                                                                                                                                                                                                      (FAMILY 11
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                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                               from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridiaceae;
                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xylanase
                                                           47;
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                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                   SMART: SM00020; Tryp_SPC: 1.
PROSITE; PS501240; TRYPSIN_DOM;
PROSITE: PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                               InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                        EMBL; X97635; CAA66231.1; -. HSSP; P00766; 1CHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98079203; PubMed-9418008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 SGTISVSK 219
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                                                                                                                                                                                                                                                                                                                                                  TRYPSIN FAMILY. ELASTASE SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 35, Created)
. 35, Last sequence upo
. 40, Last annotation upo
rsor (EC 3.4.21.71).
                                                                                                        protease;
   16
289
269
73
121
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74
222
202
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 CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
BY SIMILARITY.
BY SIMILARITY.
                                                                                            Zymogen; Signal.
BY SIMILARITY.
                                                                      ACTIVATION PEPTIDE ELASTASE 2.
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Best Local
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P45798;
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EMBL; U04836; AAA60459.1; -.
HSSP; P23904; 1AJK.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
Hydrolase; Glycosidase; Signal.
                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spilliaert R., Hreggvidsson G.O., Kristjansson J.W. Eggertsson G., Palsdottir A.; "Cloning and sequencing of a Rhodothermus marinus for a thermostable beta-glucanase and its expression and the spilling of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=21 / ITI-378;
MEDLINE=95010084; PubMed=7925416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; CFB group; NCBI_TaxID=29549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodothermus marinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coli.
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                                                                                                                                                                                                                                                                                                                                                                                                     J. Biochem. 224:923-930(1994).

J. Biochem. 224:923-930(1994).

FUNCTION: SHOWS ACTIVITY ON LICHENAN, BETA-GLUCAN AND LAMINARIN BUT NOT ON CMC CELLULOSE OR XYLAN. THE ENZYME HAS A TEMPERATURE OPTIMUM OF 85 DEGREES CELSIUS AND A PH OPTIMUM OF 7.0.

CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.

SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LETGNFTITRAD---HD------NGNNVAAY------PAIYFGC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YIAYRRTTPTTSVS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILPNNYVCYVTGWGRLQSNGALPDILQQGKLLVVDYATCSNPSWWGSTVKTNMICAGGD-
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269 /
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28856 MW;
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8343B97062CF267C CRC64;
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Matches 65
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CHAIN
ACT_SITE
ACT_SITE
SEQUENCE
                                                              EMBL; x53128; CAA37285.1; -. PIR; B43489; VGIHFS. InterPro; IPR002551; Corona_S1. InterPro; IPR002552; Corona_S2.
                                                                                                                                                                                                                                                                                                                 P18450; Q85087; Q85088;
01-NOV-1990 (Rel. 16, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA positive-strand viruses, no Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVPFS
                                Pfam; PF01600; Corona_S1;
Pfam; PF01601; Corona_S2;
                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                    modified
                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91188698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E2 glycoprotein precursor
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                                                                                                                                                                                                                                                                                                                                                                                                    Britton P., Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=11150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porcine transmissible gastroenteritis coronavirus (strain
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                                                                                                                                                                                                                                                                              TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MAND IN SYNCYTIUM FORMATION.
SUBCELLULAR LOCATION: Type I membrane protein.
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                                                                                                                                                                                    non-profit institutions as long and this statement is not removed
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158
163
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 Envelope protein;
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22.0%;
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Pred. No.
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NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
7215C33624135191 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                 Transmembrane; Signal.
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                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                    Usage
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ABFB_STRCO

O54161;

15-DEC-1998

15-DEC-1998

16-OCT-2001
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Alpha-L-arabinofuranosidase precursor
                   ABFB OR SC7H1.02
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                                                                                                                                                                                                      WD-----YATENSTWNHK--QRLNVVVNGYPYSITVTTTRNFNSAEGAIICICKGSP 137
                                                                                                                                                                                                                     WDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNV-AAYPAIYFG-- 101
                                                                                                                                                                                                                                         Similarity 23.(
45; Conservative
                                                                  STANDARD;
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N-LINKED
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CYS-RICH.
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                 87;
No.
                                        update)
                                                                475
                                                                                                                                                                                                                                                                              Actinobacteridae;
                      update)
(EC 3.2.1.55) (Arabinosidase).
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12;
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CRC64;
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CHIT_STRPL
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Best Local
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                                                                     CHIT_STRPL
P11220;
01-JUL-1989 (
01-DEC-1992 (
01-FEB-1995 (
Chitinase 63
                  Streptomyces plicatus.
Bacteria; Firmicutes; Actinobacte.
Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xylan o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstat! the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entitles requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000772; Ricin_B_lectin. Pfam; PF00652; Ricin_B_lectin; 1. SMART; SM00458; RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL021411; CAA16189.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES
-1- SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOWAIN.
                                                                                                                                                                                                                            206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-A3(2);
                                                                                                                                                                                                  282 DPT
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                                                                                                                                                                                                                                                                            154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales;
NCBI_TaxID=1902;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                     63
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                                                                                                                                                                                                                             TPT
                                                                                                                                                                                                                                                                                                                                                                      GRYRVINN--VWGAETAQCIE-VGLETGNFTITRADHDNG----
                                                                                                                                                                                                                                              SY-GSMYFSPFTNWSDMASAGQNAMNQAAVAPTLFYFAPKNIWYLAYQWGSWPFIYRTSS
                                                                                                                                                                                                                                                                      GYSGGAELMIWLNWNGGYMPGGSRVATVELAGA-----TWEVWYADWDWNYIAYRRT
                                                                                                                                                                                                                                                                                                    LPSTY---RW----
                                                                                                                                                                                                                                                                                                                                               QQWRVNSDGTVVGVESGLCLEAAGAGTANGTAVQLWTCNGGGNQKWTGLTGTPPTDGTCA
                                                                                                                                                                                                                                                                                                                      YPAIYFGCHWGACTSNSGLPRRVQELSDVRTSW-TLTPITTGRWNAAYDIWFSPVTNSGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         degradation; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                   284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50231; RICIN_B_LECTIN; 1.
                                                                     9 (Rel. 11, Created)
2 (Rel. 24, Last sequ
5 (Rel. 31, Last anno
63 precursor (EC 3.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38
39
475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                     STANDARD;
                                                                   24, Last sequence up
31, Last annotation
ursor (EC 3.2.1.14).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475
166
50045
                                                                                                                                                                                                                                                                                              SSTGV-----LAQPKSGWVALKDFTTVTHNGRHLVYGS--TSSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.9%;
                               Actinobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
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Pred. No. 5.2;
%1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycosidase; POTENTIAL.
                   Streptomycetaceae; Streptomyces.
                                                                                            update)
                                                                                                                                  610
                               Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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5.2;
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                                                                                                                                                                                                                                                                                                                                                                                                 -WSCSGGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  66;
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Best Local
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InterPro; IPR001579; Chitinase_2.
InterPro; IPR002048; EF-hand.
InterPro; IPR003961; FN_III.
InterPro; IPR001223; Glyco_hydro_18.
Pfam; PF00053; CBD_2; 1.
Pfam; PF00041; fn3; 1.
Pfam; PF00041; Glyco_hydro_18; 1.
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DOMAIN
ACT_SITE
CONFLICT
SEQUENCE
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PIR;
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J Biol. Chem. 263:443-447(1988).
-:- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-acety1-D-glucosamine polymers of chitin.
-!- INDUCTION: BY CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-45 FROM N.A., AND SEQUENCE OF 31-45.
MEDLINE-88087127; PubMed-3275646;
Robbins P. M., Albright C., Benfield B.;
"Cloning and expression of a Streptomyces plicatus chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Gene 111:69-76(1992).
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MEDLLNE-92192480; PubMed-1532161;
Robbins P.W., Overbye K., Albright
"Cloning and high-level expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M82804;
EMBL; M18397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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   347
                                                                  112
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SIMILARITY: CONTAINS
SIMILARITY: CONTAINS
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; P07986; 1EXG.
GFPDAVKNPAAFAKS-CHDLVEDPRWADVFDGIDLDWEYPNACGLSCDETSAPNAFSSMM
                                                               GLPRRVQELSDVRTSWTLTPITTGRWNAAYD----IWFSP-----VTNSGNGYSG--
                                                                                                                                 TIGDAYADYDKAYTADQSVDGVADTWDQPLRANFNQLRNLKAEYPHIKILYSFGGWTWSG
                                                                                                                                                                                                    TI - - TRADHDNG
                                                                                                                                                                                                                                                               GGDGGEPNPNPGAEVKM-GYFTNWGVYGRNYHVKNLVTSGSAEKITHINLRFGNVQGGKC 286
                                                                                                                                                                                                                                                                                                                           GDNGKEPEPEPTVELCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGNF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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PS00561; CBD_BACTERIAL; 1.
PS01095; CHITINASE_18; 1.
e; Glycosidase; Chitin degradation;
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AAA26717.1; -.
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1 BACTERIAL-TYPE CELLULOSE-BINDING
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F -> I (IN REF. 2).
; 6A202EF361CCD500 CRC64;
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Pred. No. 7
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FIBRONECTIN TYPE-III.
CATALYTIC.
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DOMAIN 17 1388
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DOMAIN 1409 1447
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CARBOHYD 26 26
CARBOHYD 26 26
CARBOHYD 94 94
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CARBOHYD
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InterPro; IPR002552; Corona_S2.
Pfam; PF01600; Corona_S1; 1.
Pfam; PF01601; Corona_S2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=92410651; PubMed=1326823;
Sanchez C.M., Gebauer F., Sune C., Mendez A., Dopazo J., Enjuanes L.;
"Genetic evolution and tropism of transmissible gastroenteritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVPPR
                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virology 190:92-105(1992).
-!- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA
Coronaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porcine transmissible gastroenteritis coronavirus (strain Pur46-MAD).
Viruses: ssRNA positive-strand viruses, no DNA stage; Nidovirales;
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15-JUL-1999
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(Rel. 28, Last sequence update)
(Rel. 38, Last annotation update)
(Rel. 38, Last annotation update)
tein precursor (Spike glycoprotein) (Peplomer protein).
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BY SIMILARITY.
EZ GLYCOPROTEIN.
EXTRACELLULAR (POTENTIAL).
                                                                                       CYS.RICH.

CYS.RICH.

RECEPTOR-BINDING (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Best Local S
Matches 51
Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K. Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saitc Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9742667;
MEDLINE-9742667; PubMed-9742667;
MEDLINE-974267; PubMed-974667;
MEDL
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15-JUL-1998
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                      Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                     C.K., Mayhew
                                                                                                                                                                                                                                                                                                                                                                              М.А.,
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    P96463;
15-DEC-1998
15-DEC-1998
16-OCT-2001
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                                                                                                           STRAIN-1326;
                                                                                                                                          Biochem.
                                                                                                                                                            Vincent P., Shareck F., Dupont C. "New alpha-L-arabinofuranosidase cloning and DNA sequence of the a
                                                                                                                                                                                               STRAIN=66 / 1326;
MEDLINE=97220396; PubMed=9148759;
                                                                                                                                                                                                                                                                Streptomyces lividans. Bacteria; Firmicutes;
                                                                                                                        REVISIONS
                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                            NCBI_TaxID=1916;
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ECOGene; EG13659; ybfM.
Hypothetical protetn; Complete prot
SEQUENCE 468 AA; 52780 MW; 954B
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EMBL; D90707; BAA35329.1; ALT_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTP-TYASSNGRLDIWW----DNRSDFNANGEKAVFFGAMYDLKNWN---LPGFAIGASY 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWL-----NWNGGVMPGGSRVATV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSVNDLYDGTAWLQALTFG------YRAADVVDLRLEGTWVKADGQQGYFLQR 327
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Streptomycineae; Streptomycetaceae; Streptomyces.
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DEGRADATION
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Exoglucanase B precursor (EC 3.2.1.91) (Exocellobiohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELF1
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SMART; SM00458; RICIN, 1.
PROSITE; PS50231; RICIN_B_LECTIN; 1.
Xylan_degradation; Hydrolase; Glycosidase; Signal; Lectin.
                                                                        MEDLINE-96003896; pubMed-7575482;
Shen H., Gilkes N.R., Kilburn D.G., Miller R.C. Jr.,
"Cellobiohydrolase B. a second exo-cellobiohydrolase
cellulolytic bacterium Cellulomonas fimi.";
                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobactactinomycetales; Micrococcineae;
                                                                                                                                                                                                                                                                                                                                                          CBHB OR CENE.
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InterPro; IPR000772; Ricin_E
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                                                                                                                                                                                                   SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                             Cellulomonas fimi.
                                                                                                                                                                                                                                                                                                                                                                          (1,4-beta-cellobiohydrolase B) (CBP120).
       SEQUENCE OF 54-75
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- SIMILARITY:
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CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.
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ococcineae; Cellulomonadaceae; Cel
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RICIN B-TYPE LECTIN.
; C3CB14EE7BF85AAD CRC64;
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915 45 Matches

Similarity

Conservative

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Query Match
Best Local
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                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94197708; PubMed-8147863; Shen H., Tomme P., Meinke A., Gil
                                                                                                                                                                       CHAIN
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PRINTS; PR00844; GLHYDRLASE48.
ProDom; PD011903; Glyco_hydro_
                                                                                                                                                                                                                                                                                          Pfam; PF00553; CBD_2; 1.
Pfam; PF00041; fn3; 3.
Pfam; PF02011; Glyco_hydro_48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
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                                                                                                                      DOMAIN
                                                                                                                                 DOMAIN
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InterPro; IPR003962; FnIII_repeat.
InterPro; IPR000556; Glyco_hydro_48.
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                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in cellulose and cellotetraose, releasing cellobiose fro
reducing ends of the Chains.
SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAIN:
SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WITH INVERSION OF ANOMERIC CONFIGURATION.

CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROLASES).
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             5.7%;
                                                                                                                                                                                                                                                                                                                                                                        CBD_2.
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                                                                                                                                                                                                              Hydrolase;
Score 82.5; Depred. No. 21; Pred. No. 21; No. 21; Pred. Mismatches
                                                                                                                               EXOGLUCANASE B.
CATALYTIC (BY SIMILARITY).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
                                                                             NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                       CELLULOSE-BINDING (BY SIMILARITY).
                                                                                                                    FIBRONECTIN TYPE-III 3.
                                                                                                                                                                                                  POTENTIAL
                                                                   046BB9D956F2F399 CRC64;
                                                                                                                                                                                                             Glycosidase;
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                           Length
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fimi: endoglucanase
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Search completed: August 15, 2002, 10:58:02 Job time: 380 sec `	1010 TNTGTTTINGWSLGEDLTAGQKVQQGWSATWTQSGSTVTATNAPWNGTLAPG 1061	149 TNSGNGYSGGAELMIWLNWNGGVMPG 174	973

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(c) 1993 - 2000 Compugen Ltd
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O9kys4 streptomyce
Q60033 thermotoga
P96492 thermotoga
O53438 mycobacteri
O94218 aspergillus
O00095 trichoderma
O13454 aspergillus
O9v2t0 pyrococcus
                                                                                                                                                     033897 rhodothermu
09kihl streptomyce
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008468 streptomyce
09rjy3 streptomyce
054331 streptomyce
09x602 streptomyce
031030 pectobacter
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Q9urr5 penicillium	Q9URR5	ω	516	6.3	90.5	ü
Q9a4b3 caulobacter	Q9A4B3	16	950	6:3	91	2
Q9xwc5 caenorhabdi	Q9XWC5	ഗ	690	6.3	91.5	Ξ
Q94bw3 cinnamomum	Q94BW3	10	580	6.3	91.5	0
Q94bw4 cinnamomum	Q94BW4	10	580	6.3	91.5	9
Q9f2z0 streptomyce	Q9F2Z0	N	348	6.4	92	8
Q93x57 fragaria an	Q93X57	10	840	6.4	92.5	37
Q9hrm4 halobacteri	Q9HRM4	17	604	6.4	93	8
~	Q9X2F7	16	443	6.5	94	5
	Q9V6J2	s	112	6.5	94	4
	Q9URR6	w	516	6.5	94.5	ຜ
	Q9URR7	w	516	6.5	94.5	2
	Q97VS7	17	322	6.6	95.5	ï
Q98kd3 rhizobium l	Q98KD3	16	213	6.6	96	õ
æ	007178	16	673	•	97	9
Q93gm7 salmonella	Q93GM7	N	809	6.8	98	8
Q9kth2 vibrio chol	Q9KTH2	16	957	6.8	99	27
	052375	N	361	7.4	106.5	6
Q9p8n6 cochliobolu	Q9P8N6	ω	239	9.4	136	5
Q97x08 sulfolobus	Q97x08	17	334	•	139	4
	Q97YG7	17	332	•	142.5	ũ
æ	Q9S5x8	16	258	•	153	ະວ
	P96491	N	257	10.6	153	1
	Q60032	N	257	•	153	õ
_	008428	N	257	•	153	6
	Q9AN41	N	263	•	156.5	8
074705 aspergillus	074705	ω	239	11.2	161.5	7

ALIGNMENTS

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01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
CELLULASE (EC 3.2.1.4).
                                                                                                                                                                                                       MEDLINE-9824392; pubMed-9581291;
MEDLINE-9824392; PubMed-9581291;
Halldorsdottir S., Thorolfsdottir E.T., Spilliaert R., Johansson M.,
Thorbjarnardottir S.H., Palsdottir A., Hreggvidsson G.O.,
Kristjansson J.K., Holst O., Eggertsson G.;
"Cloning, sequencing and overexpression of a Rhodothermus marinus gene encoding a thermostable cellulase of glycosyl hydrolase family 12.";
Appl. Microbiol. Biotechnol. 49:277-284(1998).
EMBL; U72637; AAB65594.1; -.
InterPro; IPR002594; Glyco_hydro_12.
Pfam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
Hydrolase; Glycosidase.
SEQUENCE 260 AA; 28770 MM; 94F197DB7D0D247A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-ITI378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhodothermus marinus
Bacteria; CFB group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   033897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=29549;
  61
  VWGAETAQCIEVGLETGNFTITRADHDNGNNVAAYPAIYFGCHWGA-----CTSNSGLP 114
                                    Similarity
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                 91.2%;
90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rhodothermus obamensis). Rhodothermus group; Rhodo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05,
19,
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Last sequence update)
Last annotation update)
                                                                                                              Score 1318.5; DB 2;
pred. No. 1.2e-97;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            group; Rhodothermus
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                                                                                                                                                       DB 2;
                                                                                                                Indels
                                                                                                                                                     Length
                                                                                                                                                       260;
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                                                                                                              Gaps
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RESULT
Q59963
ID Q
AC Q
DT 0
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                                                                                                                  В
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Q9KIH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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Best Local
    Q59963;
Q59963;
01-NOV-1996
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01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001230; Glyco_hydro_12.
InterPro; IPR001230; Prenyltn.
Pfam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SEQUENCE 371 AA; 38481 MW; 0E1BC4288A148914 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              van Solingen P., Meijer D., van der Kleij W.A. Bolle R., Power S.D., Jones B.E.;
"Cloning and expression of an endocellulase ge Streptomycete isolated from an East African sc Submitted (FEB-2000) to the EMBL/GenBank/DDBJ EMBL, AF233376, AAF91283.1;
HSSP, P07986; 1EXG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-11AG8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; S
NCBI_TaxID=133452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces sp. 11AG8.
Bacteria; Firmicules; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELLULASE 12A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9KIH1;
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                                                                                                                                                                                 149
                                                                                                                  208
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                                                                                                             KDFVDQAVSHGLATPDWYLTSIQAGFEPWEGGTGLAVNSFSSAV
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                                                                                                                                                                                                SVYDGCHYGNCAPRTTLPMRISSIGSAPSSVSYRYTGNGVYNAAYDIWLDP-TPRTNGVN 148
                                                                                                                                                                                                                                                                 AIYFGCHWGACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYS
                                                                                                                                                                                                                                                                                                       QICDRYGTTTIQ-DRYVVQNNRWGTSATQCINV---TGNGFEITQADGSVPTNGAPKSYP
                                                                                                                                                                                                                                                                                                                      GSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDLKAFIDDAVARGYIRPEWY
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                                                                                                                                                                                                                                                                                                                                                                            , 68
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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    (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                    PRELIMINARY;
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   01,
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                                                                                                                                                                                                                                                                                                                                                                       27;
    Created
                                                                                                                                                                                                                                                                                                                                                                     Score 396.5;
Pred. No. 6.7e
27; Mismatches
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Last sequence update)
Last annotation update)
                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomycetaceae; Streptomyces.
                                  382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371
                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
5.7e-24;
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soda lake
                                                                                                                                                                                                                                                                                                                                                                        99;
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Best Local S
Matches 77
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                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   225
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008468 PRELIMINARY;
008468;
01-JUL-1997 (TrembLrel. 0
01-JUL-1997 (TrembLrel. 0
01-DEC-2001 (TrembLrel. 1
                  halstedii JM8.";
Biochem. J. 324:
                                                       "Two genes encoding are clustered and co
                                                                                              Garda-Salas A.L., Fernandez-Abalos
Santamaria-Sanchez R.I.;
                                                                                                                            MEDLINE-97307849; PubMed-9182697;
                                                                                                                                                                                                                                                     Streptomyces halstedii. Bacteria; Firmicutes; A
                                                                                                                                                                                                                                    Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD004316; Glyco_hydro_12; 1.
PROSITE; PS00561; CBD_BACTERIAL; UNKNOWN_1.
Hydrolase; Glycosidase.
SEQUENCE 382 AA; 39398 MW; 21C014342EFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001919; CBD_2.
InterPro; IPR002594; G1yco_hydro_12
Pfam; PF00553; CBD_2; 1.
Pfam; PF01670; G1yco_hydro_12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces rochei (Streptomyces parvullus).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St.
NCBI_TaxID=1928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TremBLrel.
01-DEC-2001 (TremBLrel.
CELLULASE (EC 3.2.1.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95011642; PubMed=7523249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P07986; 1EXG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mastromei G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *Characterization and sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIQGRYVVQNNRWGTSATQCV-TATDSG-FRVTQADGSVPTNGAPKSYPSVFNGCHYTNC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVA--AYPAIYFGCHWGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAGNOWYLTSIQAGFEPWQNGAGLAVNSFSSTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNW 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGQIQPIGSQVGTASVAGRTWEVWSGGNGTNDVLSFVAPSAMSSWSFDVMDFVRATVARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGGVMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDLKAFIDDAVARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                           FROM N.A.
324:403-411(1997).
2; AAC45429.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                  Streptomycineae;
                                                       co-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39398 MW; '21C014342EFC6565 CRC64;
                                                     an endoglucanase and a cellulose-binding o-regulated by a TTA codon in Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.3%;
                                                                                                                                                                                                                          Actinobacteria; Actinobacteria; ptomycineae; Streptomycetaceae;
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04,
19,
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                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                         Created)
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Pred. No. 2.5e
32; Mismatches
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Last annotation update)
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                                                                                                                J.M.,
                                                                                                                                                                                                                                                     Actinobacteridae;
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                                                                                                                Sanchez P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 382;
                                                         Streptomyces
                                                                                                                Ruiz-Arribas
                                                                                                                                                                                                                                  Streptomyces
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Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9RJY3 PRELIMINARY;
Q9RJY3;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
InterPro; IPR001919; CBD_2.
InterPro; IPR002594; Glyco_hydro_12.
Ifam; PF00553; CBD_2; 1.
Ifam; PF01670; Glyco_hydro_12; 1.
If ProDom; PD004316; Glyco_hydro_12; 1.
If PROSITE; PS00561; CBD_BACTERIAL; UNKNOWN_1.
SEQUENCE 381 AA; 39199 MW; 97CD8FF58679E4EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-A3(2);
STRAIN-A3(2);
Cerdeno A.M., Parkhill J., E
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InterPro; IPR0019594; Glyco_hydro_12.
Pfam; PF00553; CBD_2; 1.
Pfam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
Brolog; Clyco_hydro_12; 1.
                                                                                                                                                                                                     Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; Rinashi H., Hopwood D.A.; Bet of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; AL133210; CAB61599.1; ".
HSSP; P07986; 1EXG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oliver K., Harris D.;
Submitted (NOV-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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377 AA; 388
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e EMBL/GenBank/DDBJ databases.
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Pred. No. 4.6e-20;
3; Mismatches 91;
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                                                                                                                                                                                                                Query Match
Best Local Similarity 36.9
Matches 77; Conservative
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Best Local
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Q54331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases. EMBL; 0046/39; AAB71950.1; .
HSSP; P07986; 1EXG.
InterPro; IPR001919; CBD_2.
InterPro; IPR002594; Glyco_hydro_12.
Pfam; PF00553; CBD_2; 1.
Pfam; PF01670; Glyco_hydro_12; 1.
Pfonom; PF01670; Glyco_hydro_12; 1.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
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113 TDLPVRLDTVSAAPSSISYGFVDGAVYNASYDIWLDPTARTDG--VNQTEIMIWFNRVGP
                                                     111 SGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNWNGG 170
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                                                                                                        GRYVVQNNRWGSTAPQCV-TATDTG-FRVTQADGSAPTNGAPKSYPSVFNGCHYTNCSPG 112
                                                                                                                                          GRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVA--AYPAIYFGCHWGACTSN 110
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                                                                                                                                                                                                                Score 343; DB 2;
Pred. No. 1.3e-19;
1; Mismatches 97;
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Pred. No. 8.9e-20;
1; Mismatches 97
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                                                                                                                                                                                                                                                                   Length 381;
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Best Local S
Matches 85
            O31030;
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InterPro; IPR001919; GBD_2.
InterPro; IPR002594; Glyco_hydro_12.
Ffam; PF00553; CBD_2; 1.
Pfam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
SEQUENCE 384 AA; 40918 MW; D3968
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Submitted (FEB 199) to the EMBL/GenBank/DDBJ databases.
EMBL; AF130408; AAD25090.1; -.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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32.1%; Pred.
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18,
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            sequence update)
annotation updat
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No. 3e-19;
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RESULT
OPKYS4

ID WX 94

AC Q9

AC Q9
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O1-OCT-2000 (TrEMBLrel. 1
O1-UN-2001 (TrEMBLrel. 1
PUTATIVE SECRETED SUGAR H
SC514.15
                                                                                                                   SEQUENCE FROM 1
STRAIN=A3(2);
Cerdeno A.M., 1
Submitted (MAY
                                                                                                                                                                                                                                                                  Murphy L., Harris D.;
Submitted (MAY-2000)
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacte. Actinomycetales; Streptomycineae;
   MEDLINE=97000351; PubMed=8843436;
                                                      SEQUENCE FROM N.A.
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InterPro; IPR002594; Glyco_hydro_12.
Pfam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
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SIGNAL 1
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products.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BETA(1,4)-GLUCAN GLUCANOHYDROLASE PRECURSOR CELB.
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                                                                                                                   .M., Parkhill (MAY-2000) to
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
CRETED SUGAR HYDROLASE.
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                                                                                                                      J., I
o the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinobacteria;
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                                                                                                                   Barrell B.G., Rajandream M.A.
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 242.5;
Pred. No. 8.0
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BETA(1,4)-GLUCAN GLUCANOHYDROLASE.
; 70EA3666B8443CEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carotovora subsp. carotovora LY34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomycetaceae;
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RP SEQUENCE FROM N.A.

REPLINE-99287316; PubMed-10360571;

RMEDLINE-99287316; PubMed-10360571;

RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

RA HoDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

RA Heidelberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";

RA Hature 399:323-329(199).

REMBL; 769341; CAA93274.1; -.

REMBL; 769341; CAA93274.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENDO-1.4-BETA-GLUCANASE PRECURSOR (EC 3.2.1.4) (CELLULASE)
(ENDOCIUCANASE) (CARBOXYMETHYL CELLULASE).
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Q60033;
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EMBL; AL355913; CAB91127.1; L.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MSB8 (DSM3109);
MEDLINE-96425879; PubMed-8828221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermotoga maritima.
Bacteria; Thermotogales;
NCBI_TaxID=2336;
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Pfam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thermostable cellulases, CelA and recombinant enzymes. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Greif I.;
"Analysis of a Thermotoga maritima DNA f
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microbiology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELB OR TM1525
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SEQUENCE
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILKWIKD--TKGWMGNE-TIGDVQFGYEITSSAGGLDFRTNNLTV 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bronnenmeier K., Riedel K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.18; 26.78;
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Pred. No. 8.5e-09;
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     Biochem. Biophys. Res. Commun. 194:1359-1
-i-CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF LINKAGES IN CELLULOSE.

EMBL; U93354; AAC95060.1; -.
EMBL; U93354; AAC95060.1; -.
EMBL; 286103; CAB06782.1; -.
InterPro; IPR002594; Glyco_hydro_12.
Pfam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
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Pfam; PP01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
Signal; Hydrolase; Glycosidase; Complete proteome SIGNAL 1 17
POTENTIAL.
                                                                                                                                                          STRAIN-Z706-MC24;
STRAIN-Z706-MC24;
MEDLINE-93356813; PubMed-8352795;
MEDLINE-93356813; PubMed-8352795;
                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TIEMBLIEL. 03, Created)
01-JAN-1998 (TIEMBLIEL. 05, Last sequence update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation update)
ENDO-1,4-BBTA-GLUCANNASE B (EC 3.2.1.4) (CELLULASE) (ENDOGLUCANASE)
(CARBOXYMETHYL CELLULASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P96492;
                                                                                            "Cloning and expression in Escherichia coli of Thermotoga neapolitana genes coding for enzymes of carbohydrate substrate degradation."; Biochem. Biophys. Res. Commun. 194:1359-1364(1993).
-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
                                                                                                                                                 Dakhova O., Kurepina N., Velikodvorskaya G.;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Bok J.D., Eveleigh D.
Submitted (JUN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                        SEQUENCE OF 1-137
                                                                                                                                                                                                                                                   Zverlov
                                                                                                                                                                                                                                                              STRAIN=Z2706-MC24;
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        Thermotoga neapolitana.
Bacteria; Thermotogales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSPDQTSVSSGDAEIMVWF-YNNVLMPGGQKVDEFTTTVEINGVKQETKWDVYFAPWGWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYTNSGNGYSGGAELMIWLNWNGGVMPGGSRV----ATVELAG----ATWEVWYADWDWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                           OF 1-137
                                                                                                                                                                                                                                   (MAR-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GLRSADFSVTV 260
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31734 MW;
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                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
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Pred. No. 1.5e-08;
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ENDO-1,4-BETA-GLUCANASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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WEDLINE-98295987; PubMed-9634230;
Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gole S.T., Brosch R., Gas S., Barry C.E. III, Tekala F.,
Gordon S.V., Elglmeier K., Gas S., Barry C.E. III, Tekala F.,
A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
A Hornsby T., Jagels K., Krogh A., McLean J., Murphy L.,
A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
A Rutter S., Seeger K., Skelton S., Squares R.,
A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Tomplete genome sequence.";
Complete genome sequence.";
Rature 393:537-544(1998).
EMBL; ALO21897; CAA17266.1; -.
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O53438;
O1-JUN-1998 (TIEMBLrel. 06, Created)
O1-JUN-1998 (TIEMBLrel. 06, Last sequence update)
O1-DEC-2001 (TIEMBLREL. 19, Last annotation update)
HYPOTHETICAL 16.4 KDA PROTEIN.
RV1090 OR MTV017.43.
RV1090 TABLET AND TAB
                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculist; Rv1090; -...
InterPro; IPR002594; Glyco_hydro_12.
Pfam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 151 AA; 16404 MW; 8BCC10CFFC9C8E54 CRC64;
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Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
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TNLPTEVGQILSAPTSIDYNYPTTGVWDASYDICLDSTPKTTGVN----QQEIMIWFNHQ 58
                                                                 SGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWF--SPVTNSGNGYSGGAELMIWLNWN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVELCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGNETITRADHDNGNNVAAYPA
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27.1%;
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Pred. No. 3.2e
14; Mismatches
                                                                                                                                                                                      Score 194; DB 16;
Pred. No. 3.3e-08;
6; Mismatches 78;
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000095;
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01-JUL-1997
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SIGNAL
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"A xyloglucan-specific endo-beta-1,4-glucanase from A aculeatus: expression cloning in yeast, purification characterization of the recombinant enzyme."; Glycobiology 9:93-100(1999).
EMBL: AF043595; AAD02275.1;
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Pfam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
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MEDLINE-99102417; PubMed-9884411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus aculeatus.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                          231 SEYSISIE
                                                                                                                                   254
                                                                                                                                                              172
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                                                                                                                                                                                                                  116
                                                                                                                                                                                                                                             139
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                                                                                                                                  ADFSVTVQ
                                                                                                                                                           GDTTVYSFVADSTTESFSG-DLNDFFTYLVDNEGVSDELYLTTLEAGTEPFTGSNAKLTV
                                                                                                                                                                             WDWNYIAYRRTTPTTSVSELDLKAFIDDAVARGYIRPEWYLHAVETGFELWEG-GAGLRS
                                                                                                                                                                                                                  VAYDTFLAETASGSSKY---
                                                                                                                                                                                                                                          AAYDIWFSPVTNSGNGYSGGAELMIWLNWNGGVMP---GGSRVATVELAGATWEVWYA-D 194
                                                                                                                                                                                                                                                                                              AIYFGCHWGACTSNSGLPRRVQELSDVRTSWTLTPI-----TTGRW-----N 138
                                                                                                                                                                                                                                                                                                                        DFCGQWDT--ATAGDFTLYNDLWGESAGTGSQC------
                                                                                                                                                                                                                                                                                                                                                   ELCGRWDARDVAGGRYRVINNVWGAET----AQCIEVGLETGNFTITRADHDNGNNVAAYP 96
                                                                                                                                                                                                                                                                    -----WHTSWSWSGGSSSVK--SYVNAALTFTPTQLNCISSIPTTWKWSYSGSSIVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PITDSWYLTSIRAGLEPWSDGVGLGVDSFSAKV 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSIQPVGSPVGNTTIEGKNFVVWDGSNGMNNAMAYVATEP-IEVWSFDVMSFVDHTATME
                                                                                                                                                                                                                                                                                                                                                                              63;
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              238
(TrEMBLrel.
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                          238
                                                                                                                                   261
                                                                                                                                                                                                                                                                                                                                                                                                                                              δ,
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238
                                                                                                                                                                                                                                                                                                                                                                                                                                              25158
                                                                                                                                                                                                                                                                                                                                                                                         12.3%;
04
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                                                                                                                                                                                                               -EIMVWLAALGGAGPISSTGSTIATPTIAGVNWKLYSGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                              39;
Created)
Last sequ
                                                                                                                                                                                                                                                                                                                                                                                        Score 178.5;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                             GLUCANASE.
; FCCA6746D9AEC1B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XYLOGLUCAN-SPECIFIC ENDO-BETA-1,4-
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                       234
                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                          .7e-07
                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                              ; 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64
                                                                                                                                                                                                                                                                                                                          -TGVDSYSGDTIA---
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  York W.S.,
                                                                                                                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                 171
                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                              12;
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sequence update)

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O13454
ID O13454
AC 013454
AC 013454
DT 01-DEC
DE ENDO-1
GN CELA.
OS ASPERG
OC EURCHAIY
OC
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Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        013454 PRELIMINARY;
013454;
01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
ENDO-1,4-BETA-GLUCANASE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus oryzae.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

NCBI_TaxID=5062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appl. Environ. Microbiol. 64:55-563(1998).
EMBL; AB003694; BAAA0140.1; -.
InterPro; IPR002594; Glyco_hydro_12.
Pfam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
Hydroless Glyco_hydro_12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular characterization and heterologous expression of the gene encoding a low-molec ular-mass endoglucanase from Trichoderma reesei 0M9414.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trichoderma reesei (Hypocrea jecorina).

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreales; Hypocreaceae; Hypocrea.

NCBI_TaxID=51453;
                                                            "Molecular cloning, purification and characterization of two endo-1,4-beta-glucanases from Aspergillus oryzae KBN616.";
Appl. Microbiol. Biotechnol. 46:538-544(1996).
EMBL; D83731; BAA22588.1; -.
InterPro; IPR002594; Glyco_hydro_12.
Pfam; PF01670; Glyco_hydro_12; 1.
Probom; PD004316; Glyco_hydro_12; 1.
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        Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97161783; PubMed=9008887; Kitamoto N., Go M., Shibayama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-KBN616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase;
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=QM9414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         ľsukagoshi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 CGRWDARDVAGGRYRVINNVWGAETAQ----CI-EVGLETGNFTITRAD----HDNGNNVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 28.6 les 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY----ADWDWNYIAYRRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYSG----DVKNFFNYLRDN----KGYNAAGQYVLSYQFGTEPFTGSGTLNVASWTASI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTTSVSELDLKAFI----DDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NHVTYSGDYELMIWLGKYGDIGPIGSSQGTVNVGGQSWTLYYGYNGAMQVYSFVAQTNTT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDQW--ATFTGNGYTVSNNLWGASAGSGFGCVTAVSLSGG--ASWHADWQWSGGQNNVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQ-----NSQIAIPQKRTVNSISSMPTTASWSYSG-SNIRANVAYDL-FTAANP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YPAIYFGCHWGACTSNSGLP--RRVQELSDVRT--SWTLTPITTGRWNAAYDIWFSPVIN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycosidase.
234 AA; 25159 MW; DF476EEDE384ADD1 CRC64;
        Glycosidase
239 AA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sekiya T., Yokoyama K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.2%; 28.6%;
    26096 MW;
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05,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
3.2.1.4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 176.5; DB 3; Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
COF850E5DFEB455D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Kimura T., Kito Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
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                                                                                                                                                                                                                                                                                                                                                                                          Ohmiya
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                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
 176
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                                                                                                                               09
                                                                                                                                                                97
                                                                                                                                                                                                                                40
                      YIAYRRTTPTTSVSELDLKAFIDDAVAR-GYIRPEWYLHAVETGFELWEGG 248
                                                                                                                                                                                                                 ELCGRWDARDVAGGRYRVINNVWGAET---AQCIEVGLETGNFTITRADHDNGNNVAAYP 96
TYSFVSATPINTFGG-DIKKFFDYITSKHSFPASAQYLINMQFGTEPFTGG
                                                            -FTAADQNHVTYSGDYELMIWLARYGTIQPIGTQIDTATVEGHTWELWYGTTIQAGAEQK 175
                                                                                             WESPVTNSGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY-----ADWDWN 198
                                                                                                                               AWHTTWTWNGGEGSVKSYSNSAVTFDKKLVSDVQSIPTDVEWSQDNTNVNA---DVAYDL 116
                                                                                                                                                                                                 ELCAQYDS -- ASSPPYSVNNNLWGQDSGTGSQCVYV ------DNLSSSGA-- 59
                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                               -----GACTSNSGLPRRVQEL-SDVRTSWTLTPITTGRWNAAYDI 143
                                                                                                                                                                                                                                                                             11.9%; Score 172.5;
27.3%; Pred. No. 2.
                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                               .9e-06;
                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                 86;
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                Length 239;
                                                                                                                                                                                                                                                               45;
                                                                                                                                                                                                                                                               Gaps
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Search completed: August 15, 2002, 10:57:39 Job time: 393 sec

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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Perfect score:
                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                          1106.5
470.5
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seq length: 2000000000
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                                                                                                                                                           Query
Match
  14:
16:
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                                                                                                                                                                                                                                                                           A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747574 segs, 111073796 residues
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ELCGRWDARDVAGGRYRVIN.....FELWEGGAGLRSADFSVTVQ
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1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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260
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AAB14880
AAY84345
AAY67496
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AAY06368
                                                                 AAY06367
AAY08473
                                                                                                                     AAY 06369
AAB 14882
                                                                                            AAY06342
                                                                                                      AAY84347
                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search time 53.28 Seconds (without alignments) 462.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 747574
        Emericella deserto
Amino acid sequenc
Rhodothermus marin
Streptomyces sp. E
Actinomycete sp. 3
Streptomycete livid
Amino acid sequenc
Actinomycetes cell
Protten sequence
                                                                                                                                                           Description
                                                                                                                                Rhodothermus marin
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Fusarium javanicum Amino acid sequenc	AAY84337	21	244	14.8	183
Fusarium javar	AAY06359	20	244	14.8	183
T. phaseolina	AAY44341	21	244	•	184.5
Tiarosporella	AAW68593	19	244	•	184.5
Trichoderma	AAU07582	22	234		191.5
Amino acid s	AAY84340	21	348		192.5
Gliocladium	AAB14875	21	348	15.6	192.5
Gliocladi	AAY06362	20	348		192.5
Humicola grisea E	AAY06355	20	253		192.5
Streptomyc	AAY06337	20	104	•	199
Humicola insoler	AAY06356	20	255		201.5
Humicola	AAU07583	22	254	•	$\overline{}$
Humicola	AAU07584	22	254	٠	209
Humicola gr	AAU07558	22	254		209
Amino acid	AAY84333	21	254	•	209
Humicola gr	AAB14868	21	254	•	209
Amino acid se	AAY84344	21	246		210.5
Actinomycet	AAB14879	21	246	•	210.5
Emericella de	AAY06366	20	246	•	210.5
Amino aci	AAY84334	21	254		212
Humicola in	AAB14869	21	254		212
Ø	AAY84331	21	239	•	214
	AAB14866	21	239	17.3	214
gillus	AAY06353	20	239		214
Amino acid sequenc	AAY84329	21	259	•	
gillus	AAB14864	21	259	•	
Aspergillus aculea	AAY06351	20	259	•	
Amino acid sequenc	AAY84348	21	264	•	(1)
Erwinia carotovara	AAB14883	21	264	•	10
O	637	20	264		252.5
lus lic	8846	20	261	•	10
eque	843	21	429	•	329
Rhodothermus marin	AAB14881	21	381	27.8	343

ALIGNMENTS

AAY06369 standard; Protein;

260

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RESULT
AAYO6369
ID AAYO
XX AAYO
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KW Foold
XX Foold
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cellulase; endoglucanase; EGIII; textile; feed additive; baking; food processing; grain wet milling; pulp; paper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodothermus marinus EGIII-like cellulase
                                                                                         Example; Fig 6; 47pp; English.
                                                                                                                                                                                      EGIII like cellulase
                                                                                                                                                                                                                                                                           WPI; 1999-395187/33.
                                                                                                                                                                                                                                                                                                                                                                         Bower BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY06369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEMV ) GENENCOR INT INC
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                                                                                                                                                                                                                                                                                                                                                                    Fowler T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0991720
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Streptomyces

The present polypeptide represents a full-length sequence of

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  deduced from a gene sequence isolated from genomic DNA using PCR primers (see AAX59180-91) based on conserved motifs (see AAY06325-29) of Trichoderma reesei EGIII cellulase and related enzymes. PCR has been used to identify novel EGIII-like enzymes, including the present protein, from bacterial and fungal sources (see AAY06331-70). The sequence shows homology to T. resei EGIII (see AAY06331). Also provided by the invention are vectors, host cells and methods for the recombinant production of such enzymes, which can be used in the treatment of cellulose-containing textiles, as feed additives, in the treatment of wood pulp, in the reduction of biomass to glucose, in the stone washing of indigo dyed denim, or as laundry detergent components (all claimed).
    Example 1;
                           Novel endoglucanase III or treating textiles and wood specified positions in the
                                                                                                            Mitchinson C,
                                                                                                                                                                  18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                     Emericella desertoru EGIII-like cellulase.
                                                                                                                                        (GEMV ) GENENCOR INT INC
                                                                                                                                                                                            12-NOV-1999;
                                                                                                                                                                                                                                                                          Emericella desertoru
                                                                                                                                                                                                                                                                                                                         Emericella desertoru;
                                                                                                                                                                                                                                                                                                                                                                                 21-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB14882 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDLKAFIDDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTVQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gysggaelmiwlnwnggvmpggsrvatvelagatwevwyadwdwnyiayrrttpttsvse
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                                                                                                                                                                                                                                                                                                  treatment; feed additive; detergent
  Fig
                                                                                                                                                                                                                                                                                                                 mutant;
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
    ω
••
                                                                                                             Wendt DJ;
                                                                                                                                                                  98US-0216295
                                                                                                                                                                                            99WO-US26704
52pp; English
                                                                                                                                                                                                                                                                                                                enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.7%;
                                                                                                                                                                                                                                                                                                             Trichoderma reesei; endoglucanase III;
zyme stability; textile treatment;
                           endoglucanase III-like cellulase useful for pulp comprises a substitution or deletion as wild form of endoglucanase III -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1106.5;
Pred. No. 9.6e.
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
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Best Local Similarity
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                 Novel variant endoglucanase III-like cellulases with improved surfactant stability and resistance to temperature stress, use textile processing or cleaning, treating wood pulp, food and greducing biomass to glucose .
                                                                                                                                                                                                                                                                                                                                                                 indigo
pill re
                                                                                                                                                                                                                                                                                                                                                                                             Endoglucanase III;
cellulase; textile
                                                                                                                                                                                          03-SEP-1998;
                                                                                                                                                                                                                                                        16-MAR-2000
                                                                                                                                                                                                                                                                                     WO200014208-A1
              reducing
                                                                                            WPI; 2000-271052/23.
                                                                                                                                                                                                                         24-AUG-1999;
                                                                                                                                                                                                                                                                                                                    Rhodothermus marinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of an endoglucanase III (EGIII)-like cellulase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY84347 standard; Protein; 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elcgrwdardvaggryrvinnvwgaetaqcievgletgnftitradhdngnnvaaypaiy
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                                                                                                                                                                                                                                                                                                                                                                removal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202;
                                                                                                                                                                                                                                                                                                                                              ase; textile processing; textile cleaning; stonewashing; dyed denim; cellulose containing fabric; fabric smoothness; emoval; fibril removal; cotton; cellulosic fibre; dying; det feed; wood pulp; paper; grain; biomass reduction; glucose.
              biomass to glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 AA;
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                                                                                                                                                                                          98US-0146729
                                                                                                                                                                                                                         99WO-US19154
                                                                                                                                                                                                                                                                                                                                                                                                             EGIII; EGIII-like cellulase; surfactant stability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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Pred. No. 9.6e-107;
4; Mismatches 9;
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                                food and grain,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an endoglucanase III (EGIII)-like cellulase. The cellulase has homology to the Trichoderma reesei EGII protein. The variant cellulases have improved temperature stability,
                                                                                                                                                                                                      Bower
                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9931255-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhodothermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cellulase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodothermus marinus EGIII-like cellulase (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY06342 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                    Example; Fig 3;
                                                                                     EGIII like cellulase
                                                                                                                                             WPI; 1999-395187/33
                                                                                                                                                                                                                                                                                                                16-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                        14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cellulase; endoglucanase;
food processing; grain wet
                                                                                                                                                                                                                                                        (GEMV ) GENENCOR INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ELCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVAAYPAIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDLKAFIDDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTVQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGCHWGA-----CTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ldlkafiddavargyirpewylhavetgfelweggaglrtadfsvtvq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gysggaelmiwlnwnggvmpggsrvatvelagatwevwyadwdwnyiayrrttpttsvse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fgchwaparairdcaaragavrraheld-----vtpittgrwnaaydiwfspvtnsgn 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elcgrwdardvaggryrvinnvwgaetaqcievgletgnftitradhdngnnvaaypaiy 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202;
                                                                                                                                                                                                BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                Fowler T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              marinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                97US-0991720
                                                                                                                                                                                                                                                                                                                                                                        98WO-US26552
                       47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.7%;
                                                                                                                                                                                                Phillips JI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                se; EGIII; textile; wet milling; pulp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
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Pred. No. 9.6e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6e-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              feed additive; baking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present polypeptide represents a partial sequence of a novel EGIII-like cellulase of Rhodochermus marinus. It was deduced from a partial gene sequence isolated from genomic DNA using PCR primers (see AAY06325-29) based on conserved motifs (see AAY06325-29) of Trichoderma reesei EGIII cellulase and related enzymes. PCR has been used to identify novel EGIII-like enzymes, including the present polypeptide, from bacterial and fungal sources (see AAY06331-70). Also provided by the invention are vectors, host cells and methods for the recombinant production of such enzymes, which can be used in the treatment of cellulose-containing textiles,
           The present polypeptide represents a full-length sequence of a novel EGIII-like cellulase of Streptomyces sp. 11AG8. It was deduced from a gene sequence isolated from genomic DNA using PCR primers (see AAX59180-91) based on conserved motifs (see AAY06325-29) of Trichoderma reesei EGIII cellulase and related enzymes. PCR has been used to identify novel EGIII-like enzymes, including the present protein, from bacterial and fungal sources (see AAY06331-70). The sequence shows homology to T. reesei EGIII (see AAY06330). Also provided by the invention are vectors, host cells and methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as feed additives, in the treatment of wood pulp, in the reductic of biomass to glucose, in the stone washing of indigo dyed denim, or as laundry detergent components (all claimed).
                                                                                                                                                                                                                                                             Bower BS,
                                                                                                                                                                                                                                                                                                                                                                                  24 - JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                 WO9931255-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cellulase; endoglucanase; EGIII; textile; feed additive; baking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces sp. EGIII-like cellulase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY06367 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                  Example; Fig 6; 47pp; English.
                                                                                                                                                                                                  EGIII like cellulase
                                                                                                                                                                                                                                                                                                                       16-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                    14-DEC-1998;
                                                                                                                                                                                                                                                                                        (GEMV ) GENENCOR INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            processing; grain wet milling; pulp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Similarity
87; Conserv
                                                                                                                                                                                                                                                             Fowler T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                         97US-0991720
                                                                                                                                                                                                                                                                                                                                                      98WO-US26552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.1%;
                                                                                                                                                                                                                                                             Phillips JI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 470.5;
Pred. No. 3.6e
3; Mismatches
of such enzymes,
host cells and enzymes, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .6e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             paper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                        24-JUN-1998;
19-NOV-1997;
19-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in the trea
additives,
biomass to
This invention describes a novel cellulase isolated from an Actinomycsp. which can be used in detergent compositions, as animal feeds (to increase nutritional value) and in treatment of textiles (e.g. stone washing or modifying texture, feel and/or appearance of cellulosic
                                                                                                                                                                                                                                                                                                                                                              pulp; draining
high-fructose
                                                                                                                                                                                                                                                                                                                                                                         Cellulase, detergent; animal feed; nutritional value; textile; stone washing; texture modification; appearance; cellulosic fabric; pulp; draining; paper; baking additive; starch treatment; grain;
                                                                Claim
                                                                                     New Actinomycete 
animal feeds and
                                                                                                                                    WPI; 1999-347481/29
                                                                                                                                                                                                                                                        18-NOV-1998;
                                                                                                                                                                                                                                                                                27-MAY-1999
                                                                                                                                                                                                                                                                                                                            Actinomyces sp
                                                                                                                                                                                                                                                                                                                                                                                                   Cellulase;
                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycete
                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY08473 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                   (GEMV ) GENENCOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            omass to laundry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGN-FTITRADHDNGNNVA--AYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIYFGCHWGACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qicdrygtttiq-dryvvqnnrwgtsatqcinv---tgngfeitqadgsvptngapksyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -rteimiwfnrvgpvqpigspvgtahvggrswevwtgsngsndvisflapsaisswsfdv
                                                                                                                                                           BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of cellulose-containing textiles, as feed ves, in the treatment of wood pulp, in the reduction of sto glucose, in the stone washing of indigo dyed denim, ndry detergent components (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , 68
                                                                                                                         AAV72359
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                                                             Fig 1; 36pp;
                                                                                                                                                          Van Der Kleij WAH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         sp. 36kD cellulase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                         98US-0104308.
97US-0974041.
97US-0974042.
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                                                                                                                                                                                                                                                        98WO-US24649
                                                                                                                                                                                   INT INC.
                                                                                   in treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 371
                                                                                                                                                                                                                                                                                                                                                               syrup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.1%;
                                                             English
                                                                                                                                                                                                                                                                                                                                                               production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 396.5; DB Pred. No. 1e-32;
                                                                                                                                                           Van
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                     l in detergent textiles
                                                                                                                                                          Sollingen
                                                                                                                                                                                                                                                                                                                                                                 ethanol
                                                                                                                                                          P,
                                                                                                                                                                                                                                                                                                                                                              production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                               compositions,
                                                                                                                                                          Weyler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
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                                                                                                                                                           Ξ
                                                                                                                                                                                                                                                                                                                                                             ; grain;
fibre reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371;
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                                      Actinomycete
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Best Local S
Matches 89
The present sequence is a cellulase related to endoglucanase III (EGIII) from Trichoderma reesei. EGIII-like genes were isolated from genomic DNA libraries constructed from various microorganisms by PCR. The isolated genes showed significant homology to EGIII from T. reesei. Certain substitution and deletion mutations have been incorporated into EGIII and EGIII-like cellulases to produce variant enzymes with improved stability, e.g. increased resistance to temperature stress. The mutants may be used in textile and wood pulp treatment, as a feed additive, and for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fabrics, including removal or immature or the desired as baking additing treating starch (in production of high-fructose corn syrup or treating starch (in production of high-fructose corn syrup or ethanol) and for treating grain (to reduce fibre during milling).
                                                                                                                                                                 Novel endoglucanase III or endoglucanase III-like cellulase useful for treating textiles and wood pulp comprises a substitution or deletion as specified positions in the wild form of endoglucanase III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cellulase; mutant; enzyme stability; textile treatment; wood pulp treatment; feed additive; detergent.
                                                                                                                                    Example 1; Fig
                                                                                                                                                                                                                                                         Mitchinson C,
                                                                                                                                                                                                                                                                                                                                                                              29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces lividans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces lividans; Trichoderma reesei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-2000
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                                                                                                                                                                                                                                                                                                                    18-DEC-1998;
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                                                                                                                                    3; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cellulase
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Best Local
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The present sequence represents an endoglucanase III (BGIII)-like cellulase. The cellulase has homology to the Trichoderma reesei EGIII protein. The variant cellulases have improved temperature stability, and improved surfactant stability. The variant cellulases and compositions containing them are used in textile processing or cleaning, e.g. stonewashing of indigo dyed denim, and modifying the texture, feel or appearance of cellulose containing fabrics (e.g. improving fabric
                                                                                                                                                    Novel variant endoglucanase III-like cellulases with improved surfactant stability and resistance to temperature stress, useful for textile processing or cleaning, treating wood pulp, food and grain, and reducing biomass to glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cellulase; textile processing; textile cleaning; stonewashing;
indigo dyed denim; cellulose containing fabric; fabric smoothness;
pill removal; fibril removal; cotton; cellulosic fibre; dying; detergent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biomass to glucose. They denim and as an agent in
                                                                                                                                                                                                                                                                                                                                                          24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       WO200014208-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   animal feed; wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endoglucanase III; EGIII; EGIII-like cellulase; surfactant stability;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  svydgchygncaprttlpmrissigsapssvsyrytgngvynaaydiwldp-tprtngvn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qicdrygtttiq-dryvvqnnrwgtsatqcinv---tgngfeitqadgsvptngapksyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid sequence of an endoglucanase III (EGIII)-like cellulase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 AA;
                                                                                                                       Page 64-65; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                          98US-0146729.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pulp;
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                                                                                                                                                                                                                                                                                             INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                paper; grain; biomass reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are also useful for stonewashing laundry and dish detergents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
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Best Local
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                                                                                                                                        24-JUN-1998;
18-NOV-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                smoothness or removing pills and fibrils). The compositions may also be used for the removal of immature or dead cotton from cellulosic fibres or fabric, which can cause uneven dying. The cellulase may also be used in a detergent composition for washing laundry and dishes and in the treatment of animal feed, wood pulp, paper, non-animal foods and grains. The enzymes may also be used in the reduction of biomass to glucose.
                                                                                                                                                                                                                                                                                                                                  Streptomyces
                                                                                                                                                                                                                                                                                                                                                        Cellulase; Actinomycetes; detergent; feed
pulp; paper.
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY67496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY67496 standard; protein;
                       compositions, treating
                                  A novel Actinomocyes cellulase and
                                                           N-PSDB;
                                                                                            Jones
                                                                                                                                                                                        28-MAY-1999;
                                                                                                                                                                                                              24-FEB-2000
                                                                                                                                                                                                                                    WO200009707-A1
                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetes cellulase protein sequence.
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                                                                                                                  (GEMV ) GENENCOR INT INC
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                                                         2000-224344/19.
DB; AAZ57029.
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                                                                                           Van Der Kleij
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                        98US-0104308.
98WO-US24649.
99US-0321981.
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                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.1%;
                                                                                                                                                                                                                                                                                  "signal sequence"
                        textiles
                                                                                                                                                                                                                                                            "mature protein"
                                                                                            WAH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371
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                                                                                            Van
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                       and paper or pulp
                                  related DNA, useful
                                                                                            Solingen
                                                                                                                                                                                                                                                                                                                                                                       additive; textile treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
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                                                                                            Weyler
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                                   for
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                                  detergent
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Claim 1;

Fig

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ARESULT
AAX 6749

ID AX 6749

AC AF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                               24-JUN-1998;
18-NOV-1998;
28-MAY-1999;
A novel Actinomocyes cellulase and related DNA, useful compositions, treating textiles and paper or pulp -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7497
                                                                                                                                                                Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cellulase; Actinomycetes; detergent; pulp; paper; cellulase 11AG8.
                                                                                                                                                                                                                                                                                                                                                                   28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200009707-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces lividans.
                                                                                                                                                                                                             (GEMV ) GENENCOR INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protien sequence of CelA and cellulase 11AG8 fusion
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                                                                                    2000-224344/19
DB; AAZ57031.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAFIDDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIYFGCHWGACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qicdrygtttiq-dryvvqnnrwgtsatqcinv---tgngfeitqadgsvptngapksyp
                                                                                                                                                             BE,
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89; Conservative
                                                                                                                                                           Van Der Kleij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                            98US-0104308.
98WO-US24649.
99US-0321981.
                                                                                                                                                                                                                                                                                                                                                                   99WO-US11971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "celA signal sequence" 47..386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.1%; Score 396.5; DB 21; 39.7%; Pred. No. 1e-32; tive 27; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "cellulase 11AG8 mature peptide"
                                                                                                                                                           WAH,
                                                                                                                                                           Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                           Solingen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        feed additive; textile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   = - = :=
                                                                                                                                                      Weyler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                            for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371;
                          detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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RESULT 1
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                          WPI; 1999-395187/33.
                                                                                                                                                                                                                                                                              Streptomyces lividans.
                                                                                                                                                                                                                                                                                                                    Cellulase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides a cellulase from Actinomycetes. The cellulase can be used in a detergent composition, as an additive for animal feed and for the treatment of textiles or pulp and paper. The DNA encoding the cellulase can be used to identify homologous cellulases and for recombinant production of cellulases. The present sequence represents the protein sequence of a cell signal sequence and cellulase llAGB fusion sequence contained in the expression cassette consisting of the GI promoter, cell signal sequence, cellulase llAGB and GI terminator
                                                          Example;
                                                                                  EGIII like cellulase
                                                                                                                                                                                  16-DEC-1997;
                                                                                                                                                                                                         14-DEC-1998;
                                                                                                                                                                                                                                 24 -JUN-1999
                                                                                                                                                                                                                                                         WO9931255-A2
                                                                                                                                                                                                                                                                                                                                           Streptomyces lividans EGIII-like cellulase
                                                                                                                                                                                                                                                                                                                                                                    06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                            AAY06368;
                                                                                                                                                         (GEMV ) GENENCOR INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                    AAY06368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 -rteimiwfnrvgpvqpigspvgtahvggrswevwtgsngsndvisflapsaisswsfdv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qicdrygtttiq-dryvvqnnrwgtsatqcinv---tgngfeitqadgsvptngapksyp 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAFIDDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAELMIWLNWNGGYMPGGSRVATVELAGATWEVWYADWDWNYIAYRTTPTTSVSELDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       svydgchygncaprttlpmrissigsapssvsyrytgngvynaaydiwldp-tprtngvn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIYFGCHWGACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYS 117
                                                                                                                                  BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kdfvdqavshglatpdwyltsiqagfepweggtglavnsfssav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89;
                                                        Fig 6; 47pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                 Fowler T,
                                                                                                                                                                                                                                                                                                                   endoglucanase; EGIII; textile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 15; 72pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                 97us-0991720.
                                                                                                                                                                                                         98WO-US26552.
                                                                                                                                                                                                                                                                                                      grain
                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.1%; Score 396.5; DB 2 39.7%; Pred. No. 1.1e-32;
                                                          English
                                                                                                                                 Phillips
                                                                                                                                                                                                                                                                                                      wet milling; pulp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                  ï;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                      paper
                                                                                                                                                                                                                                                                                                                    feed
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                                                                                                                                                                                                                                                                                                                  additive;
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                                                                                                                                                                                                                                                                                                                  baking;
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5

The present polypeptide represents a full-length sequence of a novel EGIII-like cellulase of Streptomyces lividans (CelB). It deduced from a gene sequence isolated from genomic DNA using pc primers (see AAX59180-91) based on conserved motifs (see AAY063

PCR It was

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RESULT
AAB14881
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Trichoderma reesei EGIII cellulase and related enzymes. PCR has been used to identify novel EGIII-like enzymes, including the present protein, from bacterial and fungal sources (see AAY06331-70). The sequence shows homology to T. reesei EGIII (see AAY06330). Also provided by the invention are vectors, host cells and methods for the recombinant production of such enzymes, which can be used in the treatment of cellulose-containing textiles, as feed additives, in the treatment of wood pulp, in the reduction of biomass to glucose, in the stone washing of indigo dyed denim, or as laundry detergent components (all claimed).
 The present sequence is from Trichoderma reesei
                                                                                                                                                                                                                                                                                                                                               Rhodothermus marinus; Trichoderma reesei; endoglucanase III; EGIII; cellulase; mutant; enzyme stability; textile treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                             Novel endoglucanase III or endoglucanase III-like cellulase useful for treating textiles and wood pulp comprises a substitution or deletion at
                                                                                                                      WPI; 2000-482483/42.
                                                                                                                                               Mitchinson C,
                                                                                                                                                                                                     18-DEC-1998;
                                                                                                                                                                                                                                                                                                           Rhodothermus marinus.
                                                                                                                                                                                                                                                                                                                                                                                                                    21-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB14881 standard; Protein;
                                      Example 1; Fig 3; 52pp; English.
                                                                                                                                                                        (GEMV ) GENENCOR INT INC.
                                                                                                                                                                                                                              12-NOV-1999;
                                                                                                                                                                                                                                                         29-JUN-2000
                                                                                                                                                                                                                                                                                  WO200037614-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 PEWYLHAVETGFELWEGGAGLRSADFSVTVQ 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 ndwyltsvqagfepwqngaglavnsfsstve 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNWNGG 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gryvvqnnrwgstapqcv-tatdtg-frvtqadgsaptngapksypsvfngchytncspg 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iqpigspvgtasvggrtwevwsggngsndvlsfvapsaisgwsfdvmdfvratvarglae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
77; Conser
                                                                textiles and wood positions in the
                                                                                                                                                                                                                                                                                                                                    treatment; en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                          marinus
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                Wendt DJ;
                                                                                                                                                                                                    98US-0216295.
                                                                                                                                                                                                                              99WO-US26704.
 reesei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.8%;
                                                                                                                                                                                                                                                                                                                                     feed
                                                                                                                                                                                                                                                                                                                                                                                          EGIII-like cellulase.
            a
 t cellulase
EGIII-like
                                                                                                                                                                                                                                                                                                                                     stability; additive;
                                                                pulp
wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 343; DB 20;
Pred. No. 3.8e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        æ
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                                                                 form
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related to
genes were
                                                                                                                                                                                                                                                                                                                                    detergent.
                                                                 of endoglucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97;
 endoglucanase isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6;
III (EGIII)
genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                               at
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              libraries constructed from various microorganisms by PCR. The isolated genes showed significant homology to EGIII from T. reesel. Certain subsitution and deletion mutations have been incorporated into EGIII and EGIII-like cellulases to produce variant enzymes with improved stability, e.g. increased resistance to temperature stress. The mutants may be used in textile and wood pulp treatment, as a feed additive, and for reducing blomass to glucose. They are also useful for stonewashing or indigo dyed denim and as an agent in laundry and dish detergents.
                                                                                                                                                                                                                                                                                                                                                                                         cellulase; textile processing; textile cleaning; stonewashing; indigo dyed denim; cellulose containing fabric; fabric smoothness; pill removal; fibril removal; cotton; cellulosic fibre; dying; detergent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                     Novel variant endoglucanase III-like cellulases with improved surfactant stability and resistance to temperature stress, useful for
                                                                                                                                    WPI; 2000-271052/23
                                                                                                                                                                  Fowler T;
                                                                                                                                                                                                                            03-SEP-1998;
                                                                                                                                                                                                                                                         24-AUG-1999;
                                                                                                                                                                                                                                                                                                                 WO200014208-A1
                                                                                                                                                                                                                                                                                                                                               Streptomyces lividans.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Endoglucanase III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of an endoglucanase III (EGIII)-like cellulase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY84346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY84346 standard; Protein;
                                                                       textile processing
                                                                                                                                                                                              (GEMV ) GENENCOR INT INC
                                                                                                                                                                                                                                                                                     16-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 ndwyltsvqagfepwqngaglavnsfsstve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVA--AYPAIYFGCHWGACTSN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tdlpvrldtvsaapssisygfvdgavynasydiwldptartdg--vnqteimiwfnrvgp 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gryvvqnnrwgstapqcv-tatdtg-frvtqadgsaptngapksypsvfngchytncspg 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               iqpigspvgtasvggrtwevwsggngsndvlsfvapsaisgwsfdvmdfvratvarglae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNWNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDLKAFIDDAVARGYIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                            98US-0146729.
                                                                                                                                                                                                                                                        99WO-US19154.
                                                           ç
                                                                                                                                                                                                                                                                                                                                                                        pulp; paper; grain; biomass
                                                              or cleaning,
                                                                                                                                                                                                                                                                                                                                                                                                                                        EGIII; EGIII-like cellulase; surfactant stability;
                                                         glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 343; DB 21;
Pred. No. 3.8e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                         treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
                                                                         wood pulp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 381;
                                                                          food
                                                                       and grain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191
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Disclosure;

Page 65-66; 73pp;

English.

present sequence

represents an

endoglucanase III (EGIII)-like

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RESULT :
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cellulase. The cellulase has homology to the Trichoderma reesei EGIII protein. The variant cellulases have improved temperature stability, and improved surfactant stability. The variant cellulases and compositions containing them are used in textile processing or cleaning, e.g. stonewashing of indigo dyed denim, and modifying the texture, feel or appearance of cellulose containing fabrics (e.g. improving fabric smoothness or removing pills and fibrils). The compositions may also be used for the removal of immature or dead cotton from cellulosic fibres or fabric, which can cause uneven dying. The cellulase may also be used in a detergent composition for washing laundry and dishes and in the treatment of animal feed, wood pulp, paper, non-animal foods and grains. The enzymes may also be used in the removal be used in the removal feed, wood pulp, paper, non-animal foods and grains.
New enzyme preparation comprising a xyloglucanase with an activity
                                 WPI; 1999-120866/10
N-PSDB; AAX06949.
                                                                            Bjornvad ME,
                                                                                                                                      24-OCT-1997;
07-JUL-1997;
                                                                                                                                                                                   01-JUL-1998;
                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                 Bacillus
                                                                                                                                                                                                              21-JAN-1999.
                                                                                                                                                                                                                                           WO9902663-A1
                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus licheniformis xyloglucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW88462 standard;
                                                                                                        (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                            Xyloglucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 laendwyltsvqagfepwqngaglavnsfsstve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 VAGGRYRVINNVWGAETAQCIEVGLETGNETITRADHDNGNNVA--AYPAIYFGCHWGAC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIRPEWYLHAVETGFELWEGGAGLRSADFSVTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spgtdlpvrldtvsaapssisygfvdgavynasydiwldptartdg--vnqteimiwfnr 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vfngchytqnnrwgstapqcv-tatdtg-frvtqadgsaptngapksypsvfngchytnc 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vgpiqpigspvgtasvggrtwevwsggngsndvlsfvapsaisgwsfdvmdfvratvarg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGGVMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDLKAFIDDAVARG
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                                                                                                                                                                                                                                                                                                                                                 licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                           Jorgensen
                                                                                                                                      97DK-0001213
97DK-0000822
                                                                                                                                                                                                                                                                                                                                                                         detergent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                   98WO-DK00290
                                                                                                                                                                                                                                                                    /note= "mature protein, this region
    claimed in Claim 19"
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.7%; Score 329; DB 21; 35.0%; Pred. No. 1.3e-25;
                                                                           PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261
                                                                           Outtrup H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 101;
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                                                                           Schuelein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                   specifically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This polypeptide is an alkaline xyloglucanase obtained from Bacillus licheniformis ATCC 14580. The enzyme shows optimal activity at 60 deg C, and retains 50% of its activity after 20 min at 70 deg. The optimum pH for activity is 5.54, with 32% relative activity retained at pH 4.59, and 45% at pH 8.49. The kcat is 16.5/sec on xyloglucan at pH 7.5% km 1.1 g/l. The ratio of maximum xyloglucanase activity to maximum activity on CM-cellulose is at least 5:1. An isolated polynucleotide (see AAX06949) encoding the xyloglucanase can be utilised in the production of recombinant enzyme. Xyloglucanase preparations are useful for improving the properties of cellulosic fibres, yarn, (non)woven fabric, and for ratting hemp, jute, flax and linen fibres (claimed). They can also be used in a process for machine treatment of fabrics, and in detergent compositions (claimed). The enzyme preparations exhibit high xyloglucanase activity at alkaline pH without essentially attacking cellulose or cellulose derivatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                               Erwinia carotovora
                                                                                                                                                                                                                            Cellulase; endoglucanase; EGIII; textile; food processing; grain wet milling; pulp;
                              (GEMV ) GENENCOR INT
                                                                16-DEC-1997;
                                                                                              14-DEC-1998;
                                                                                                                                                                                                                                                                             Erwinia carotovora EGIII-like cellulase.
                                                                                                                                                                                                                                                                                                               06-SEP-1999
                                                                                                                                                                                                                                                                                                                                               AAY06370;
                                                                                                                                                                                                                                                                                                                                                                              AAY06370 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 50 % at pH 7 - useful for improving the properties of cellulosic fibres, yarn, (non)woven fabric, and ratting hemp, jute, flax and linen fibres \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 29; Page 71-72; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                       175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 RYRVINNVWGAETA----QCIEVGLETGNFTITRADHD-----NGNNVAAYPAIYF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDLKAFIDD-AVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTVQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elmiwln-ntnagpagsyvetvsigghswkvykgyidagggkgwnvfsfirtantqs-an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELMIWLNWNGGVMPGGSRVATVELAGATWEVW--YAD----WDWNYIAYRRTTPTTSVSE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gwhwtegytagsgfptrlsdqknintkvsysisangtynaaydiwlhntnkaswdsaptd 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCHW-GACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kyyifnnvwgadqvsgwwqti-----yhnsdsdmgwvwnwpsntstvkaypsivs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                            (first entry)
                                                             97US-0991720
                                                                                              98WO-US26552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                              264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 255.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       paper
                                                                                                                                                                                                                                             feed additive; baking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261;
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9;

Bower BS,

Fowler T,

Phillips JI;

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Search completed: August 15, 2002, 10:51:03 Job time: 257 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present polypeptide represents a full-length sequence of a covel EGIII-like cellulase of Erwinia carotovora. It was deduced from a gene sequence isolated from genomic DNA using PCR primers (see AAX59180-91) based on conserved motifs (see AAY06325-29) cof Trichoderma reesei EGIII cellulase and related enzymes. PCR has been used to identify novel EGIII-like enzymes, including the present protein, from bacterial and fungal sources (see AAY06331-70). The sequence shows homology to T. reesei EGIII (see AAY06330). Also provided by the invention are vectors, host cells and methods for the recombinant production of such enzymes, which can be used in the treatment of cellulase-containing textiles, as feed additives, in the treatment of wood pulp, in the reduction of blomass to glucose, in the stone washing of indigo dyed denim, or as laundry detergent components (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 20.5%; Score 252.5; DB 20; Length 264; Best Local Similarity 31.6%; Pred. No. 5.9e-18; Matches 72; Conservative 39; Mismatches 86; Indels 31;
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                                                                                                      nirhftdylvqtkqwmsdekyissvefgteifggdggiditewrvdvk 264
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(c) 1993 - 2000 Compugen Ltd
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US-09-104-308-1

US-09-321-981-5

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US-09-110-959A-2

US-09-216-295-2

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US-09-216-295-13

US-08-438-870-10

US-08-438-870-10

US-08-438-870-3

US-09-216-295-13

US-08-438-870-10

US-08-438-870-10

US-08-438-870-3

US-09-216-295-13

US-08-448-933-34

US-08-382-452D-34

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SULT 2 -09-216-295-21 sequence 21, Application US/09216295 satent No. 6268328 seneral INCORMATION: APPLICANT: Mitchinson, Colin APPLICANT: Wendt, Dan J. TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions FILE REFERENCE: GC555	1 ELCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGNETITRADHDNGNNVAAYPAIY 60	Sequence 23, Application US/09216295 Sequence 23, Application US/09216295 Patent No. 6268328 GENERAL INFORMATION: APPLICANT: Mitchinson, Colin APPLICANT: Mendt, Dan J. TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions FILE REFERENCE: GC555 CURRENT FILING DATE: 1998-12-18 NUMBER OF SED ID NOS: 41 SOFTWARE: FastSED for Windows Version 3.0 SEO ID NO 23 LENGTH: 260 TYPE: PRT ORGANISM: Rhodothermus marinus S-09-216-295-23 Query Match Best Local Similarity 88.6%; Pred. No. 3e-102; Matches 202; Conservative 4; Mismatches 9; Indels 13; Gaps 2;	28 176.5 14.3 234 4 US-09-216-295-3 Sequence 3, Appli 30 167 13.5 237 4 US-09-216-295-15 Sequence 15, Appl 31 166.5 13.5 234 4 US-09-216-295-19 Sequence 19, Appli 31 166.5 13.5 234 4 US-09-216-295-4 Sequence 4, Appli 32 163.5 13.2 239 4 US-09-216-295-6 Sequence 6, Appli 33 163.5 13.2 250 4 US-09-216-295-6 Sequence 6, Appli 34 163.5 13.2 250 4 US-09-216-295-8 Sequence 14, Appli 35 162.5 13.2 239 3 US-08-913-264-1 Sequence 1, Appli 37 162.5 13.2 239 3 US-08-913-264-1 Sequence 1, Appli 38 161.5 13.1 239 4 US-09-216-295-12 Sequence 2, Appli 39 161.5 13.1 239 4 US-09-215-242-1 Sequence 2, Appli 41 159.5 13.0 319 3 US-08-913-264-1 Sequence 2, Appli 42 140 11.3 288 3 US-09-215-295-12 Sequence 12, Appli 43 140 11.3 288 3 US-09-215-295-12 Sequence 2, Appli 140 11.3 288 3 US-09-215-295-11 Sequence 2, Appli 140 11.3 288 3 US-09-215-295-11 Sequence 2, Appli 140 11.3 288 3 US-09-215-295-11 Sequence 2, Appli 150-5 150 150 150 150 150 150 150 150 150 15

FILE REFERENCE:

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CURRENT FILING DATE: 1998-12-18
NUMBER OF SEO ID NOS: 41
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 21
LENCTH: 312
TYPE: PRT
                                                                                                                       COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,308
FILING DATE: 24-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,042
FILING DATE: 19-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC539
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Best Local Similarity
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                                                   TELEFAX: 650-845-6504
NFORMATION FOR SEQ ID NO: 1:
                                   SEQUENCE CHARACTERISTICS:
                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 650-846-7555
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MEDIUM TYPE: Diskette
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APPLICANT: Van Solingen, Piet
APPLICANT: Weyler, Walter
TITLE OF INVENTION: No. 6187577el Ce
TITLE OF INVENTION: Cellulase Produc
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LENGTH:
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STATE: California
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US-09-104-308-1
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US-09-321-981-1
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CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: PET/US99/11971
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 09/104,308
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 08/974,042
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-19
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SEQ ID NO 1
LENGTH: 371
TYPE: PRT
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Best Local S
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                 178 KAFIDDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTV
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VENTION: No. 6287839el Cellulase Producing Actinomycetes
VENTION: Cellulase Produced Therefrom and Method of Prod
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thermovebaceous
32.1%; Score 396.5; 39.7%; Pred. No. 1.5
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US-09-321-981-5
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CURRENT APPLICATION NUMBER: US/09/321,981

CURRENT FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: PCT/US99/11971

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 09/104,308

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 08/974,042

PRIOR FILING DATE: 1997-11-19

PRIOR FILING DATE: 1997-11-19
                                      SOFTWARE: Fas
SEQ ID NO 22
LENGTH: 381
TYPE: PRT
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Best Local Similarity
Matches 89; Conserv
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SEQ ID NO 5
LENGTH: 386
TYPE: PRT
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ORGANISM: Streptomyces lividans CelB-09-216-295-22
                                                                                                                       CURRENT APPLICATION NUMBER: US/09/216,295
CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                        APPLICANT: Mitchinson, Colin APPLICANT: Wendt, Dan J. TITLE OF INVENTION: NO. 6268: FILE REFERENCE: GC555
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VENTION: No. 6287839el Cellulase Producing Actinomycetes
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; PRIOR FILING DATE: 1997-10-28; NUMBER OF SEQ ID NOS: 14; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 2; LENCTH: 261; TYPE: PRT; ORGANISM: Bacillus licheniformis ATCC 14580 US-09-110-959A-2
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Best Local :
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Best Local Similarity
Matches 77; Conserv
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-07-28
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PRIOR FILING DATE: 1297-07-07
PRIOR APPLICATION NUMBER: 121
PRIOR FILING DATE: 1997-10-24
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APPLICANT: Outtrup, Helle
APPLICANT: Jorgensen, Per
APPLICANT: Bjornvad, Mads
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PRIOR FILING DATE: 1997-10-28
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CURRENT FILING DATE: 1998-07-07
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APPLICANT: Bjornvad, Mads Eskelund
TITLE OF INVENTION: Alkaline xyloglucanase
FILE REFERENCE: 5206.200:US
                                         175 LDLKAFIDD-AVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTVQ 222
                                                                                       155 EIMIWLN-NTNAGPAGSYVETVSIGGHSWKVYKGYIDAGGGKGWNVFSFIRTANTQS-AN 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 VMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDLKAFIDDAVARGYIR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 TDLPVRLDTVSAAPSSISYGFVDGAVYNASYDIWLDPTARTDG--VNQTEIMIWFNRVGP 170
213 LNIRDFTNYLADSKQWLSKTKYVSSVEFGTEVFGGTGQINISNWDVTVR 261
                                                                                                                              121 ELMIWLNWNGGVMPGGSRVATVELAGATWEVW--YAD----WDWNYIAYRRTTPTTSVSE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 NDWYLTSVQAGFEPWQNGAGLAVNSFSSTVE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 GWHWTEGYTAGSGFPTRLSDQKNINTKVSYSISANGTYNAAYDIWLHNTNKASWDSAPTD 154
                                                                                                                                                                                                       62 GCHW-GACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGA 120
                                                                                                                                                                                                                                                                45 KYYIFNNVWGADQVSGWWQTI-----YHNSDSDMGWVWNWPSNTSTVKAYPSIVS 94
                                                                                                                                                                                                                                                                                                                                                     Local Similarity 30.0 ies 70; Conservative
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                                                                                                                                                                                                                                                                                                          15 RYRVINNVWGAETA----QCIEVGLETGNFTITRADHD-----NGNNVAAYPAIYF 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60/063,694
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                                                                                                                                                                                                                                                                                                                                                     Score 255.5; DB 4;
Pred. No. 9.1e-18;
1; Mismatches 85;
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 261;
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RESULT

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RESULT 9
US-09-216-295-24
; Sequence 24, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
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; Sequence 12, Application US/08032848C
; Patent No. 5475101
                                                                                                                                                                                                                                   밁
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APPLICANT: Mitchinson, Colin
APPLICANT: Wendt, Dan J.
TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: HORD, Margaret A.
REGISTRATION NUMBER: 33,401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 742-7356
TELEPHONE: 415 742-7217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT: Lorch, Jeffrey D.
TITLE OF INVENTION: Purification and Molecular Cloning
TITLE OF INVENTION: EG III Cellulase
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMpatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                              186 NIRHFTDYLVQTKQWMSDEKYISSVEFGTEIFGGDGQIDITEWRVDVK 233
                                                                                                                                                                                                                                                        176 DLKAFIDDAV-ARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTVQ 222
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                                                                                                                                                                                                                                                                                                                                                                                                             69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 RYRVINNVWGAETAQ------CIEVGLETGNFTITRADHDNGNNVAAYPAIYFGCH 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                   IWLNDTNAG--PAGDYIETVFLGDSSWNVFKGWINNADNGGGWNVFSFVHTSGTNSAS-L
                                                                                                                                                                                                                                                                                                                                                             IWLN-WNGGVMPGGSRVATVELAGATWEV---WYADWD----WNYIAYRRTTPTTSVSEL 175
                                                                                                                                                                                                                                                                                                                                                                                                        WTAGYTENSGLPIQLSSNKSITSNVTYSIKATGTYNAAYDIWFHTTDKANWDSSPTDELM 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGA-CTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H: 233 amino acids
amino acid
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Weiss, Geoffrey L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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      Compositions
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NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Ver.
SEQ ID NO 5
LENGTH: 259
TYPE: PRT
ORGANISM: Aspergillus aculeatus
US-09-216-295-5
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; CURRENT APPLICATION NUMBER: US/09/;
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Ver: 580 ID NO 24
; SEQ ID NO 24
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Erwinia carotovara
US-09-216-295-24
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Best Local Similarity
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US-09-216-295-5
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/216, 295
CURRENT FILING DATE: 1998-12-18
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APPLICANT: Wendt, Dan J.
TITLE OF INVENTION: No. 6268
    184
                                                                                    125
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                                                                                                                 111 NSGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY-ADWDWNYIAYRRTTPT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 DLKAFIDDAV-ARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTVQ 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 IWLNDTNAG--PAGDYIETVFLGDSSWNV-FKGWINADNGGGWN-VSFVHTSGTNSAS-L
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                                                                                                                                                                                                                 55 AYPAIYFGCHWGACTSNSGL---PRRVQELSDVRTSWTLTPITTG-RWNAAYDIWFSPVT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 KYYLFNNVWGKDEIKGWQQTIFYNSPISMG---WNWHWPSSTH----SVKAYPSLVSGWH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 RYRVINNVWGAETAQ------CIEVGLETGNFTITRADHDNGNNVAAYPAIYFGCH 64
                                                                                                                                                                                                                                                            20 QLCDQY--ATYTGGVYTINNNLWGKDAGSGSQCTTVNSASSAGTSWSTKWNWSGGENSVK 77
                                                                                                                                                                                                                                                                                                    1 ELCGRWDARDVAGGRYRVINNVWGAET---AQCIEV--GLETGNFTITRADHDNG-NNVA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIRHFTDYLVQTKQWMSDEKYISSVEFGTEIFGGDGQIDITEWRVDVK
                                            TSVSELDLKAFID-----DAVARGYIR------PEWYLHAVETGFE 204
                                                                                                                                                                       SY-----ANSGLTFNKKLVSQISQIPTTARWSYDNTGIRADVAYDLFTAADI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IWLN-WNGGVMPGGSRVATVELAGATWEVWYADW------DWNYIAYRRTTPTTSVSEL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WGA-CTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELM 123
TSF-QGDVNDFFKYLTQNHGFPASSQYLITLQFGTEPFTGGPATLSVSNWSASVQQAGFE
                                                                                  NHVT-WSGDYELMIWLARYGGVQPIGSQIATATVDGQTWELWYGANGSQKTYSFVAPTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                  18.2%; Score 224.5; DB 4
29.6%; Pred. No. 1.1e-14;
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                                                                                                                                                                                                                                                                                                                                              36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 246; DB 4; Length 263; Pred. No. 8.1e-17;
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    242
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RESULT 12
US-08-032-848C-13
; Sequence 13, Ap
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; SEQ ID NO 7
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Aspergillus kawachii (2)
US-09-216-295-7
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US-09-216-295-7
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Best Local Similarity
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CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mitchinson, Colin APPLICANT: Wendt, Dan J.
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
                                                                                                                                                                                                     APPLICANT: Lorch, Jeffrey D.
TITLE OF INVENTION: Purification and
TITLE OF INVENTION: EG III Cellulase
                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 -- ANPITSF-QGDINDFFKYLTQNHGFPASSQYLIILALQFGTEPFTGGPATLNVADWSA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 RRTTPTTSVSELDLKAFIDDAVA-RGYIRPEWYL--HAVETGFELWEGG-AGLRSADFSV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 ADINHVT-WSGDYELMIWLARYGGVQPLGSQIATATVEGQTWELWYGVNGAQKTYSFVA- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 PYTNSGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY----ADWDWNYIAY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 PWQNGAGLAVNSFSSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 LWEGGAGLRSADFSVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 TVQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 AYPAIYFGCHWGACTSNSGL---PRRVQELSDV----RTSWTLTPITTGRWNAAYDIWFS 107
                                                         ZIP: 94080
                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QLCDQY--ATYTGGVYTINNNLWGKDAGSGSQCTTVNSASSAGTSWSTKWNWSGGENSVK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ELCGRWDARDVAGGRYRVINNVWGAET---AQCIEV--GLETGNFTITRADHDNG-NNVA 54
                                                                                                                                                                                                                                                                                                                                                                  3, Application US/08032848C
5475101
                                                                                             South San Francisco CA
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                                                                             USA
                                                                                                                                                                                                                                                                                     Clarkson, Kathleen
Weiss, Geoffrey L.
                                                                                                                                                                                                                                                                                                                          Ward, Michael
                                                                                                                                                                                                                                                                   Larenas,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 6268328el Variant EGIII-Like Cellulase Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.3%;
32.1%;
                                                                                                                                                                                                                                                                     Edward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                             Molecular Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84; Indels
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                                                                                                                                                                                                                          ; ORGANISM: Humicola insolens US-09-216-295-10
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                                                                                                                                                                                                                                                               SOFTWARE: Fa:
SEQ ID NO 10
LENGTH: 253
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09216295 Patent No. 6268328
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Best Local Similarity
Matches 73; Conserv
                                                                                                                                 Matches
                                                                                                                                               Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/216,295
CURRENT FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mitchinson, APPLICANT: Wendt, Dan
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 415 742-7356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 TSF-QGDVNDFFKYLTQNHGFPASSQYLITLQFGTEPFTGGPATLSVSNWSASVQ 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 NHVT-WSGDYELMIWLARYGGVQPIGSQIATATVDGQTWELWYGANGSQKTYSFVAPTPI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 TSVSELDLKAFIDDAVA-RGYIRPEWYLHAVETGFELWEGG-AGLRSADFSVTVQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 NSGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY-ADWDWNYIAYRRTTPT 169
62 SY-----ANSGLTFNKKLVSQISQIPTTARWSYDNTGIRADVAYDLFTAADI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 AYPAIYFGCHWGACTSNSGL---PRRVQELSDVRTSWTLTPITTG-RWNAAYDIWFSPVT 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: MAR 1
                                                       37 ELYGYW-----SGNGYELLNNLWGKDTATSGWQCTYLDGTNNGGIQWSTAWEWQGAPDNV 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                          1 ELCGRWDARDVAGGRYRVINNVWGAETA----QCIEV-GLETGNFTITRADHDNG--NNV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ELCGRWDARDVAGGRYRVINNVWGAET --- AQCIEV -- GLETGNFTITRADHDNG-NNVA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
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NUMBER: 33,401
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MAR 17 1993
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31.1%; Pred. No. 1.2e-13;
40. Mismatches 92;
                                                                                                                           17.2%; Score 212; DB 4; L
30.9%; pred. No. 1.8e-13;
Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colin
                                                                                                                                                                 Length 253;
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FILE REFERENCE: GC555
CURRENT APPLICATION NUMBER: US/09/216,295
CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 253
TYPE: PRT
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Best Local Similarity
Tatches 71; Conserve
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US-09-216-295-20
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                                                                                                                                         Sequence 9, Application US/09216295
Patent No. 6268328
GENERAL INFORMATION:
APPLICANT: Mitchinson, Colin
APPLICANT: Wendt, Dan J.
TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions
FILE REFERENCE: GC555
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CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 246
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Patent No. 6268328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mitchinson, Colin APPLICANT: Wendt, Dan J.
ORGANISM: Humicola grisei
                                                                                                                                                                                                                                                                                                                                                                                                              177
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                                                                                                                                                                                                                                                                                                                                          233 DATLTVSSYSVSV 245
                                                                                                                                                                                                                                                                                                                                                                         209 GAGLRSADFSVTV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VANVAYDLF----TSSSAGGDSEYEIMIWLAALGGAGPISSTGSSIATVTLGGVTWSLYS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 IRDFSCDIKDFFNYLERNHGYPAREQNLIVYQVGTECFTGGPARFTCRDF 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --NAAYDIWFSPVTNSGNGYSGAELMIWLNWNGGVMP---GGSRVATVELAGATWEVWY 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DECGQWDTATV--GNEIVYNNLWGQDNA---DSGSQTG------VDSANGNSIS----- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTS 171
                                                                                                                                                                                                                                                                                                                                                                                                             GPNGSMQVYSFVA----SSTTESFSADLMDFINYLAENQGLSSSQYLTHVQAGTEPFTGT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSYPYVGKQIQRG-----RKISDINSMRTSVSWTYDR-TDIRANVAYDVFTARDPD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----WHTTWSWSGGSSSVKSYANAAYQFTSTKLNSLSSIPTSW-----KWQYSTTDI 120
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                                                                    for Windows Version 3.0
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28.18;
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Pred. No. 2.5e-13;
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Best Local Similarity
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191
                           163 YRRTTPTTSVSEL--DLKAFIDDAVA-RGYIRPEWYLHAVETGFELWEGG-AGLRSADF 217
                                                        133
                                                                                    103 DIWFSPYTNSGNGYSGGAELMIWLNWNGGYMPGGSRVATVELAGATWEVWYADWDWNYIA 162
                                                                                                                  75
                                                                                                                               37
                                                                                                                                                                                         1 ELCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVAAYPAIY 60
                                                     YSFLPPSGDIRDFSCDIKDFFNYLERNHGYPAREQNLIVYQVGTECFTGGPARFTCRDF 249
                                                                                                                                                                          ELYGYW-----SGNGYELLNNLWGKDTA-----TSGWQCTYLDGTNNG-----
                                                                                                                 -GIQWNTAWEWQGAPDNVKNYPYVGKQIQRGRKISDINSMRTSVSWTYDR-TDLRANVAY 132
                                                                                                                                                                                                                                    68;
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                                                                                                                                                                                                                                                  16.9%;
28.5%;
                                                                                                                                                                                                                                    31; Mismatches
                                                                                                                                                                                                                                                  Score 209; DB 4;
Pred. No. 3.6e-13;
                                                                                                                                                                                                                                                                 Length 253;
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Search completed: August 15, 2002, 10:52:08
Job time: 172 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    352
252.252.2
213
200.5
119.4
163.5
1153
142.5
139.9
95.5
93.5
93.5
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Gene 90, 9-14, 1990
A;Title: CelS: a novel endoglucanase identified from Erwinia carotovora subspace poly 9-14, 1990
A;Title: CelS: a novel endoglucanase identified from Erwinia carotovora subspace polyseries of 100328; MUID:90337352
A;Accession: JU0328
A;Molecule type: DNA
A;Residues: 1-264 <SAA>
A;Cross-references: GB:M32399; NID:9148389; PIDN:AAA24817.1; PID:9148390
A;Cross-references: GB:M32399; NID:9148389; PIDN:AAA24817.1; PID:9148390
A;Experimental source: strain SCC3193
A;Note: part of this sequence, including the amino end of the mature protein. C;Genetics:
A;Genetics:
A;Genetic
                                                                                                                                                                                                                                                                                                                                                                               Cellulase (EC 3.2.1.4) precursor - Aspergillus aculeatus
N;Alternate names: endo-1,4-beta-glucanase
C;Species: Aspergillus aculeatus
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jul-2000
C;Accession: S12610; S14118; S40186; JQ0458
R;Ooi, T; Shinmyo, A; Okada, H; Murao, S.; Kawaguchi, T.; Arai, M.
Nucleic Acids Res. 18, 5884, 1990
A;Title: Complete nucleotide sequence of a gene coding for Aspergillus acule
A;Reference number: S12610; MUID:91016934
A;Accession: S12610
A;Molecule type: DNA
A;Residues: 1-237 <COII>
A;Rocession: S127- SUNT: FORCEG: NTR. 2017010, DTRN. DRANAGES 1. DTRN. 2017810
A;Rocession: S127- SUNT: FORCEG: NTR. 2017010, DTRN. DRANAGES 1. DTRN. 2017810
                                                                                                                                                                                                        A;Cross-references: EMBL:D00546; NID:g217818; PIDN:BAA00435.1; PID:g217819 R;Ool, T.; Shinmyo, A.; Okada, H.; Hara, S.; Ikenaka, T.; Murao, S.; Arai, Curr. Genet. 18, 217-222, 1990 A;Title: Cloning and sequence analysis of a cDNA for cellulase (FI-CMCase) A;Reference number: S14118; MUID:91064758 A;Accession: S14118
A; Molecule type: protein
A; Residues: 17-18; 42-49, 'X', 51-54, 'X'; 66-79; 90-111; 136-205, 'XX', 208-211
C; Genetics:
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                                                                                       A; Cross-references: A; Accession: S40186
                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-237 <0012>
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A;Introns: 138/2; 212/1
C;Function:
C;Function:
A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such A;Pathway: cellulose degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation; pyroglutamic acid F;1-16/Domain: signal sequence #status predicted <SIG>F;17-237/Product: cellulase #status experimental <MAT>
F;17/Modified site: pyrrolidone carboxylic acid (Gin) (in mature form) #status experimental control of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-274 <ARN>
A;Cross-references: GB:AE001800; GB:AE000512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Evidence for lateral A;Reference number: A72200; Mt A;Accession: A72241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endoglucanase - Thermotoga maritima (strain MSB8)
C; Species: Thermotoga maritima
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C; Accession: A72241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain MSB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Nelson, K.E.; Clayton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 399, 323-329,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNVKSYEG-----ETWLKFDGEKVEFYADLYNIVLQNPD----SWVHGYPEIYYGYKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVAAYPAIYFGCH-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NHVT-WSGDYELMIWLARYGGVQPIGSQIATATVDGQTWELWYGANGSQKTYSFVAPTPI
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TPMKEGKVKINVKDFVQKAAEVVKKHSTRID---NFEELYFCVWEIGTEFGDPNTTAAKF
                                                                                  TPTTSVS-ELDLKAFIDDA----VARGYIRPEWYLHAVETGFELWEGGA---
                                                                                                                                                                                                                                                                                                                            WAG--HNSGVEFLPVKVKDLPDFYVTLDYSIWYENNLPI----NLAMETWITRSPDQTS
                                                                                                                                                                                                                                                                                                                                                                                                  WGACTSNSG---LPRRVQELSD--VRTSWTL----TPITTGRWNAAYDIWFSPVTNSGN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY - ADWDWNYIAYRRTTPT
                                                                                                                                                            VSSGDAEIMVWF-YNNVLMPGGQKVDEFTTTVEINGVKQETKWDVYFAPWGWDYLAFRLT
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31.1%;
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MUID:99287316
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Pred. No. 1e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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cellulase (EC 3.2.1.4) precursor - Aspergillus niger
N; Alternate names: carboxymethylcellulase I; endo-1,4-beta-glucanase
C; Species: Aspergillus niger
C; Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C; Accession: S55931; $60657; JS0730
R; Sakamoto, S; Tamura, G; Ito, K; Ishikawa, T; Iwano, K; Nishiya, N.
Curr. Genet. 27, 435-439, 1995
A; Title: Cloning and sequencing of cellulase cDNA from Aspergillus kawachii and its expr.
A; Reference number: S55931; MUID:96059347
A; Accession: S55931
A; Molecule type: mRNA
A; Residues: 1-239 <SAK>
A; Cross-references: EMBL:D12901; NID:9217812; PID:9217813
A; Note: the source is designated as Aspergillus kawachii
A; Accession: S60657
A; Molecule type: protein
A; Residues: 76-86;176-186 <SAK2>
A; Note: the source is designated as Aspergillus kawachii
C; Function:
A; Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce
C; Reywords: blocked amino end; glycosidase; hydrolase; polysaccharide degradation
C; Reywords: blocked amino end; glycosidase; hydrolase; polysaccharide degradation
F;1-16/Domain: signal sequence #status predicted <MAT>
F;17-239/Product: cellulase #status predicted <MAT>
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987
A;Accession: H70895
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Residues: 1-151 <COL>
A; Cross-references: GB:
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: H70895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWF--SPVTNSGNGYSGGAELMIWLNWN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIRPEWYLHAVETGFELWEGGAGLRSADFSVTV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GWTFRDFSVEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PITDSWYLTSIRAGLEPWSDGVGLGVDSFSAKV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSIQPVGSPVGNTTIEGKNFVVWDGSNGMNNAMAYVATEP-IEVWSFDVMSFVDHTATME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGVMPGGSRVATVELAGATWEVWYADWDW-NYIAYRRTTPTTSVSELDLKAFIDDAVARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNLPTEVGQILSAPTSIDYNYPTTGVWDASYDICLDSTPKTTGVN----QQEIMIWFNHQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:AL021897; GB:AL123456;
ce: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rv1090 - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.7%; Score 194; DI
33.3%; Pred. No. 1.90
tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
.9e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316 A;Accession: H72240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE001800; GB:AE000512; NID:g4982090; A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Garrett, M.M.; Stewart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Nelson, K.E.; Clayton, R.A.; Gill,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endoglucanase -
                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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240
                                     214
                                                                          182 LAFRLKDPVKKGRVKFDVRHFLDAAGKALSSSARVKDFEDLYFTVWEIGTEF--GSPETK
                                                                                                                                                        123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 SPINSWSG-DIKDFFNYLTQNQGFPASSQHLITLQCGTEPFTGGPATFTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112
                                                                                                               161 IAYRRTTPTTSVS-ELDLKAFIDDA-----VARGYIRPEWYLHAVETGFELWEGGAGLR
                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
                                                                                                                                                                                                                                                                       53 VAAYPAIYFGCH-WGACTS-NSGLPRRVQELS--DVRTSWTLTPITTGRWNAAYDIWFSP 108
                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 YPAIYFGCHWGACTSNSGL---PRRVQELSDVRTSWTLTPITTG-RWNAAYDIWFSPVTN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 MCSQYDS--ASSPPYSVNQNLWGEYQGTGSQCVYVDKLSSSGASWHTKWTWSGGEGTVKS
                                                                                                                                                                                                                                                                                                                                                                                                                    TM1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LCGRWDARDVAGGRYRVINNVWG---AETAQCIEVG--LETGNFTITRADHDNG-NNVAA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY-----ADWDWNYIAYRRT 166
SAQF 243
                                     SADF
                                                                                                                                                    EKYQTEASIGDVEIMVWFYFN-NLTPGGEKIEEFTIPFVLNGESVEGTWELWLAEWGWDY
                                                                                                                                                                                         VTNSGNGYSGGAELMIWLNWNGGVMPGGSR-----VATVELAGATWEVWYADWDWNY 160
                                                                                                                                                                                                                                VLGYPEFYYGYKPWENHTAEGSKLPVPVSSMKSFSVEVSFDIHHEPSLPLNFAMETWLTR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPTTSVSELDLKAFIDDAVA-RGYIRPEWYLHAVETGFELWEGGAGLRSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHATSSGDYELMIWLARYGSVQPIGKQIATATVGGKSWEVWYGTSTQAGAEQKTYSFVAG
                                                                                                                                                                                                                                                                                                               51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-258 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H72240
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                   217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SNSGLTFDKKLVSDVSSIPTSVTWSQDDTNVQADVSYDL-FTAANA 122
                                                                                                                                                                                                                                                                                                                               12.48; 27.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Gill, S.R.; Gwinn, |
Cotton, M.D.; Pratt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                             24; Mismatches
                                                                                                                                                                                                                                                                                                                             Score 153; DB 2
Pred. No. le-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 163.5;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.L.; Dodson, R.J.;
, M.S.; Phillips, C.
                                                                                                                                                                                                                                                                                                               87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.; Haft, D.H.; Hi
C.A.; Richardson,
                                                                                                                                                                                                                                                                                                             Gaps
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                                                                          239
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                                                                                                                                                      181
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Awayez, M. goc, H.P.;

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submitted to GenBank, April 2001
A; Description: Sulfolobus solfatar
A; Reference number: A99139
A; Accession: G90291
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-332 <KUR>
A; Cross-references: GB: AE006641; N
C; Genetics:
A; Gene: SS01354
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G90360
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A; Accession: G90360
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Matches 60
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Best Local Similarity
 207
                                     112
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                                                                                                                                                                                                                                     Local Similarity
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                                                                                            CH-WGACTSNSGLPRRVQELSDVRTSWTLT------PITTGRWNAAYDIWFSPVTN 111
PGN---GDIEIMVWL-FSQNLQPAGQQVGEVVIPIYINHTLVNATFQVWKMKNVPWGGWE
                                   SGNGYSGGAELMIWLNWNGGVMPGGSRVATV-----ELAGATWEVW---YADW-DWN 159
                                                                     RKPWDTSYAGNIFPMRIGNMTPFMVSFYINLTKLDPSINFDIASDAWIVRPQIAFSPGTA
                                                                                                                                                                               NVWGAETAQCIEVGLETGNFT----ITRA------DHDNGNNVAAYPAIYFG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIAYRRTTPTTSVSELDLKAFIDDA--VARGYI--RPEWYLHAVE-----TGFEL--W 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKPWDTAYAGNIFPMRIGNWTPFWVSFYINLTKLDPSINFDIASDAWIVRPQIAFSPGTA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WNAKNYNGNYTMVFNPL----ARTLSV-----SFNLTQVKPLEWTNG-----YPEIYVG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRA---DHDNGNNVAAYPAIYFG 62
                                                                                                                                           NMWNAKT-----WNGNYTMVFNPLTRTLSVSFNLTQVNPLQWTNG----YPEIYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGN---GDIEIMVWL-FSQNLQPAGEQVGKVVVPIYINHTLVNATFQVWEMKSVPWGGWE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGNGYSGGAELMIWLNWNGGVMPGGSRVATV-----ELAGATWEVW---YADW-DWN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CH-WGACTSNSGLPRRVQELSDVRTSWTLT------PITTGRWNAAYDIWFSPVTN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60;
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                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB:AE006641; NID:g13814564; PIDN:AAK41590.1; GSPDB:GN00155
                                                                                                                                                                                                                                     11.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDGWKVTNGYVSYEPNLFIKALSNFTSYNITNYYLTDW
                                                                                                                                                                                                                                   Score 139; DB 2;
Pred. No. 0.00021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 142.5; DB 2
Pred. No. 0.00011;
                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                    69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76;
                                                                                                                                                                                                                                                  Length 334;
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                                                                                                                                                                                                                  88;
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                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Awayez, M.
goc, H.P.;
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                                                                                                                                             146
 262
                                                                                                                                                                                                                  16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chan
                                           probable peptidase - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: B70528
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamris, D.; Gord, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroy, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete generate common and probable preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-673 <COL>
A;Cross-references: GB:296796; GB:AL123456; NID:93261797; PIDN:CAB09571.1; PID:9326
C;Genetics:
A;Gene: Rv0
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                                 A; Experimental source: strain H37Rv
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oostsubmitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE006641; NID:g13815835; PIDN:AAK42663.1; GSPDB:GN00155 C;Genetics:
A;Gene: celB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision
C;Accession: H90425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-322 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A99139
A; Accession: H90425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: Sulfolobus solfatarious complete genome
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Best Local Similarity
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11
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                                                                                                                                                                                                                  GLPRRVQELSDVRT--SWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNWNG 130
                                                        VPIGYILKNMGSYIEKAGVNIYNVNTYYLDAIQVGME 299
                                                                         E-----:DLKAFIDDAVARGYIRPEWYLHAVETGFE 204
                                                                                                                            NLSHTPYFIYVGNMSIPTLINGKIENLSWEVYVLPRTGSANGWTGVYFLSPLKEPKAEFG
                                                                                                                                                             G-----DWDWNYIAYRTTPTTSVS
                                                                                                                                                                                               SLPMIVLRLPNFYSILNYSYYLINGSIDDFSYDIMLSQNPNITSLQYGDFEIMIMMYWNE
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                                                                                                                                                                                                                                                                        IGYALGNVNMTININYLHVAINLSQISKISSNVVDGYPGLMYGQELWWPFMYRTTQLQFL 142
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                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                             7.78;
20.38;
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                                                                                                                                                                                                                                                                                                                                                             Score 95.5;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                            Mismatches
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Van der Oost,
                                                                                                                                                                                                                                                                                                                                                                                DB
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Oost, J.
                                                                                                                                                                                                                                                                                                                                            95;
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PIDN:CAB09571.1; PID:g32617

complete

Holroyd,

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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed R;Reference number: A69250; MUID:98049343
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein AF2119 - Archaeoglobus fulgidus
c;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
C;Accession: G69514
R;Kleik, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-741 <KLE>
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Matches
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Best Local Similarity
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                                                                                                                                                                   320 VRVNWYVDENSVLKPYPIPVVQKFTGNR----
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                                                                                    372 YGNFDDADWDGACIAVGSTTP 392
                                                                                                                                                                                                                                                     261 LSDKLRVNFVAKIEDVMTNCNAYTTTNRAILAENVAITPGSYDITLVGRMYYSGGAD-W 319
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                                                                                                                                                                                                                                                                                                                                                                    ETGNETITRADHDNGNNVAAYPA------IYFGCHWGACTSNSG------LPRR--
                                                                                                                                                                                                                                                                                                                                     DTDTTTLYAKVVSNGNPVPDYPVKFYAEFDSQRIFLG---GAWTNSSGIAKLSFIPKNVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGWHTQAMREGRDKVAQDFAAVATDLVTRGITTA------EQLGARGGS--
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                                                                                                                         ----ADWDWNYIAYRRTTP 168
                                                                                                                                                                                                           IWLNW----NGGVMP------GGSRVATVELAGATWEVWY-----
                                                                                                                                                                                                                                                                                           ------VQELSDVRTSWTLTPITTGRWNAAYDIWFSP----VTNSGN-GYSGGAELM 123
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                                                                                                                                                                                                                                                                                                                                                                                                                             49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 93.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                 -ASVTIWKYGLDDYCTDPNCHREGI 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDRVHPGHARKMTAALQAAGHPVW
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                                                                                                                                                                                                                                                                                                                                                                                                                         51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 741;
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C;Accession: B87611

R;Nelson, K,E; Eisen, J.; Heidelberg, R;Nierman, W,C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K,E; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Y70G10A.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27357
R;Lloyd, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, October 1998
A;Reference number: Z20354
A;Accession: T27357
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-690 <MILL>
A;
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B87611
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C;Genetics:
A;Gene: CC2924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A87249; A; Accession: B87611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
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A; Introns: 61/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: clone Y70G10A C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-950 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TonB-dependent receptor [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross - references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP: Y70G10A.3
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Best Local Similarity
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                                                                                                                                                434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 TYMDENVSQKASPVYLAIHAVLTSF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 AFIDDAVARGYIRPEWYLHAVETGF 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 VNDLTNQTDFGQCANRDDPECAGKPHSSWFNPYFWMFILGQTLHGVGSTPLFSIG----T 201
                                                                      48 -DNGNNVAAYPAIYFGCHWGACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWF 106
                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31
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                                                                                                                                                                                                                  2 LCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADH----
                                                                                                                                            LTGEWQVSD----KLRVDGH------IGQETSDYDIPISDKFYTEAFGGLITDYR 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSWYDFAVLLVVFPVCHWGNNGHKGR-----WIGWGGVIMALGSLICALPHWMVDIYHPD 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGYGACTPSWLQGFHNAKCLLVVLGICAFIQSFVVNAIFPVGLSTLERRFKMTSTHTGII 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:AE005673; NID:g13424546; PIDN:AAK24886.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL:AL032660; PIDN:CAA21751:1; GSPDB:GN00021; CESP:Y70G10A.3
---YKWNTTDANN---YRAHEI-DFSATYQTTELKNAEFNAAYDFSD 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ELAGATWEVWYADWDWNYIAYRR----TTPTTSVSELDLK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.48;
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                                                                                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                                                                                                                                   Score 91;
Pred. No.
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Pred. No. 5;
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7.8;
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                                                                                                                                                                                                                                                                                                   64;
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NAIternate names: xylanase B
C; Species: Clostridium acetobutylicum
C; Species: 30-Sep-1993 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999
C; Accession: S12745
R; Zappe, H.; Jones, W.A.; Woods, D.R.
Nucleic Acids Res. 18, 2179, 1990
A; Title: Nucleotide sequence of a Clostridium acetobutylicum P262 xylanase gene (xynB).
A; Reference number: S12745; MUID:90245673
A; Accession: S12745
A; Molecula type: DNA
A; Residues: 1-261 <2APP
A; Cross-references: EMBL:M31726; NID:g144933; PIDN:AAA23287.1; PID:g144934
A; Experimental source: strain P262
C; Genetics:
A; Gene: xynB
C; Function:
A; Pathway: xylan degradation
C; Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C; Keywords: extracellular protein; glocosidase; hydrolase; polysaccharide degradation
F; 12-261/Droduct: endo-1,4-beta-xylanase B #status predicted <MAT>
F; 32-255/Domain: endo-1,4-beta-xylanase bomology <xYL>
F; 152,242/Active site: Glu #status predicted
F; 152,242/Active site: Glu #status predicted
Search completed: August 15, 2002, 10:51:40 Job time: 179 sec
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                                                                                                                                                                                                                      153 YYIVDSWGSWRPPGGTSKGTITVDGGIYDIYETTRINQPSIQGNTTFKQY-WSVRRTKRT 211
                                                                                                                                                                                                                                                                        122 LMIWLNWNGGVMPGGSRVATVELAGATWEVW------YADWDWNYIAYRRT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 ADFSVT 220
                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                               99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 YRVINNVWGAETAQCIEVGLETG-NFTITRADHDNGN-----NVAAYPAIYFGCHWGAC 68
                                                                                                                                                                                                                                                                                                                                                                      TSNSG--LPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNS-----GNGYSGGAE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLTLKGGLSYRGFKNEGYSQTNDDVNRTAWERGTLDNRLDGVTKVFT-QHDDQSWII--V 582
                                                                                                                           SGTISVSK 219
                                                                                                                                                                          TPTTSVSE 174
                                                                                                                                                                                                                                                                                                                                                                                                                           YSAFNTQAAPKTITSNEIGVNGGYDYELWK---DYGNTSMTLKNGGA----FSCOW--- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPVTNSG-----NGYSGGAELMIWLNWNGGV----MPGGSRVATVELAGATWEVWYA 154
                                                                                                                                                                                                                                                                                                                          -SNIGNALFRKGKKFNDTQTYKQL----GNISVNYDCNYQPYGNSYLCVYGWTSSPLVE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68; Indels 47; Gaps
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein -
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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
            252.5

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16.313

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THTR_FOLIO
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XYN2_MAGGR
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                                                                                                                                                                                                                        EMBL; D00546; BAA00435.1; --
EMBL; X52525; CAA36757.1; --
PIR; JQ0458; JQ0458.
PIR; S12610; S12610.
PIR; S14118; S14118.
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01-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Endoglucanase I precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
(Cellulase) (FI-CMCASE).
Aspergillus aculeatus.
                                                      InterPro; IPR002594; Glyco_hydro_12.
Pfdam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
Cellulose degradation; Hydrolase; Glycosidase; SIGNAL 1 16 POTENTIAL.
CHAIN 17 237 ENDOGLUCANASE I.
                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions modelified and this statement is not removed. Usage by and for comentities requires a license agreement (see http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ooi T., Shinmyo A., Okada H., Murao S., "Complete nucleotide sequence of a gene aculeatus cellulase (FI-CMCase).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-F-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ooi T., Shinmyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91064758; PubMed=2249253;
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MISCELLANEOUS: WILL ALSO HYDROLYSE 1,4-LINKAGES IN BETA-D-GLUCANS
ALSO CONTAINING 1,3-LINKAGES.
SIMILARITY: BELONGS TO CELLULASE FAMILY H (FAMILY 12 OF GLYCOSYL
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     25560 MW;
  ENDOGLUCANASE I.
PYRROLIDONE CARBOX:
8F173571A8AE6931
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                               CARBOXYLIC
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Matches 63
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Best Local !
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Q12679;
01-NOV-1997
                                                                                                 Pfam; PF01670; Glyco_hydro_12; 1.
Probom; PD004316; Glyco_hydro12; 1.
Cellulose degradation; Hydrolase; Glycosidase;
SIGNAL 1 16 POTENTIAL.
                                                                                                                                                                                               use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                              Sakamoto S., Tamura G., Ito K., Ishikawa T., Iw "Cloning and sequencing of cellulase cDNA from and its expression in Saccharomyces cerevisiae. Curr. Genet. 27:435-439(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus. NCBI_TaxID=105351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Endoglucanase A precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase
(Cellulase A) (Carboxymethylcellulase) (CMCase-I).
                                                                                              SIGNAL

    -i- FUNCTION: HAS CARBOXYLMETHYLCELLULASE ACTIVITY.
    -i- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic

                                                                    SEQUENCE
                                                                                                                                                                      EMBL; D12901; BAA02297.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96059347; PubMed-7586029;
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SIMILARITY: BELONGS TO CELLULASE FAMILY H (FAMILY 12 OF GLYCOSYL
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              Similarity
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239 /
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25769 MW;
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              Score
Pred.
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MCSQYDS---ASSPPYSVNQNLWGEYQGTGSQCVYVDKLSSSGASWHTKWTWSGGEGTVKS

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Q48846;
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00132; GLHYDRLASE2.
PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1;
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X82287; CAA57730.1; -. HSSP; P00722; 1BGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its content is in no way mon-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96118231; PubMed-8574399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-DCT-2001 (Rel. 40, Last annotation update)
Beta-galactosidase large subunit (EC 3.2.1.23) (Lactase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001649; Glyco_hydro_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       actobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     actobacillus sakei.
                                                                                 342
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                             67
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                                                                                                             GRYRVINNV----WGAETAQCIEVGLETGNFTITRADHDNGNNVAAYP---AIYFGCHWG
GKRLVINGVNRHEWHPETGRTITAEDEAWDIACMQRNHINAVRTSHYPDRLSFYNGC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPINSWSG-DIKDFFNYLTQNQGFPASSQHLITLQCGTEPFTGGPATFTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY-----ADWDWNYIAYRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPTTSVSELDLKAFIDDAVA-RGYIRPEWYLHAVETGFELWEGGAGLRSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHATSSGDYELMIWLARYGSVQPIGKQIATATVGGKSWEVWYGTSTQAGAEQKTYSFVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y-----SNSGLTFDKKLVSDVSSIPTSVTWSQDDTNVQADVSYDL-FTAANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YPAIYFGCHWGACTSNSGL---PRRVQELSDVRTSWTLTPITTG-RWNAAYDIWFSPVTN
                                                                                                                                                                                                                                                                                                                                            465 465
533 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                    465
533
72457
                                                                                                                                                                                                            7.5%;
                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                   39;
                                                                                                                                                                                                            Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                              PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
; C658A3C46136B886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            625
                                                                                                                                                                                                               0
                                                                                                                                                                                                            DB 1;
0.81;
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                                                                                                                                                                                   87;
                                                                                                                                                                                                                                  Length 625
                                                                                                                                                                                   Indels
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                                                                                                                                                                                   76;
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                                                                                                                                                                                 Gaps
                                                                            398
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                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat.
Hypothetical protein AF2119 precursor.
AF2119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artlach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 5
                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                         Hypothetical protein; Signal; Complete proteome SIGNAL 1 22 POTENTIAL.
                                                                                                                                                                                                                                                                             TIGR; AF2119;
                                                                                                                                                                                                                                                                                         EMBL; AE000958; AAB89151.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-VC-16 / DSM 4304 / ATCC 49
MEDLINE-98049343; PubMed-9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YL19_ARCFU
                                                   204 DTDTTTLYAKVVSNGNPVPDYPVKFYAEFDSQRIFLG---GAWTNSSGIAKLSFIPKNVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               556 DMYQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 ELWEGG
                   78
                                                                                      36
------VQELSDVRTSWTLTPITTGRWNAAYDIWFSP----VTNSGN-GYSGGAELM 123
                                                                                     ETGNFT ITRADHDNGNNVAAYPA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEYKATISDVESRMYATPAEIKAYLDNAPQKPFILCE-YMHDMGNSLGGMQSYIDLLSQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----TSVSEL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILFW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DQAGIYMMAETNLESHGSWQKMGAVEPSWNVPGSYDEWEAATLDRARTNFETFKNHV
                                                                                                                                    Similarity
                                                                                                                                                                                                         741 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209
                                                                                                                      Conservative
                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                        741
82084 MW;
                                                                                                                                    7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---DLKAFIDDAVARGYIRPEWYLHAVETG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SLGNESYAGSVLEKMNA-----YYKQQDPTRLVHYEGVFRA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / ATCC 49558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaeoglobales; Archaeoglobaceae;
                                                                                                                    21;
                                                                                                                    Score 93; DB
Pred. No. 0.98
%1; Mismatches
                                                                                                                                                                                                        HYPOTHETICAL PROTEIN AF2119: E8C7543552231583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                     ----IYFGCHWGACTSNSG-----LPRR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              741 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                    DB 1
                                                                                                                                                      1;
                                                                                                                      51;
                                                                                                                                                    Length 741;
                                                                                                                      0,0
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                                                                                                                   Gaps
                                                     260
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                                                                 Query Match
Best Local Similarity
                                                      Matches
                                                                                                                                      CHAIN
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p17137;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Endo-1.4-beta-xylanase precursor (EC 3.2.1.8)
                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electropean Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90245673; pubMed=2336398;
Zappe H., Jones W.A., Woods D.R.;
"Nucleotide sequence of a Clostridium acetobutylicum P262
gene (xynB).";
                                                                                                                         SEQUENCE
                                                                                                                                                                                                                               InterPro; IPR001137; Glyco_hydro_11,
Pfam; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GLHYDRLASE11.
                                                                                                                                                                                                                                                                      PIR; S12745; S12745.
HSSP; P36217; 1XYO.
                                                                                                                                                                                                                                                                                                  EMBL; M31726; AAA23287.1;
                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Fi
Clostridium
                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 18:2179-2179(1990).
-1- CATALYTIC ACTIVITY: Endohydrolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XYNA_CLOSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-169679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xylan xylanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261
  50
                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linkages in xylans.
PATHWAY: XYLAN DEGRADATION.
SIMILARITY: BELONGS TO CELLULASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                               CAUTION: Was originally thought to originate from
                                                                                                                                                                                                                                                                                                                                                                                                                                  C.acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYDROLASES).
                          YRVINNVWGAETAQCIEVGLETG-NFTITRADHDNGN-----NVAAYPAIYFGCHWGAC 68
YSAFNTQAAPKTITSNEIGVNGGYDYELWK---DYGNTSMTLKNGGA----FSCQW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGNFDDADWDGACIAVGSTTP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRVNWYVDENSVLKPYPIPVVQKFTGNR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ADWDWNYIAYRRTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IWLNW----NGGVMP------GGSRVATVELAGATWEVWY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSDKLRVNFVAKIEDVMTNCNAYTTTNRAILAENVAITPGSYDITLVGRMYYSGGAD-W
                                                                                                                                                                                         degradation;
                                                                                                                                                                                      PS00776; GLYCOSYL_HYDROL_F11_1; 1. PS00777; GLYCOSYL_HYDROL_F11_2; 1. gradation; Hydrolase; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Firmicutes;
                                                                                                                      29
152
242
261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          saccharobutylicum.
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                      261
152
242
                                                                                                                         29032
                                                                 7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                         ¥.
                                                     28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168
                                                                Score 88.5; DB Pred. No. 0.77;
                                                                                                                     ENDO-1, 4-BETA-XYLANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONG (BY SIMILARITY).;
339C3616F6FD14AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261
                                                                                                                                                                                                                                                                                                                                                             There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 1,4-beta-D-xylosidic
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                                                                            DB 1;
                                                                                                                                                                                         Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G
                                                     68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Xylanase) (1,4-beta-D-
                                                                              Length
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                          EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xylanase
                                                     47;
                                                                                                                                                                                                                                                                                                                                                                                             a collaboration -
MBL outstation -
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PIR; B43489; VGIHFS.

InterPro; IPR002551; Corona_S1.

InterPro; IPR002552; Corona_S2.

Pfam; PF01600; Corona_S1; 1.

Pfam; PF01601; Corona_S2; 1.
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                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmissible gastroenteritis virus.";
Virus Res. 18:71-80(1990).
-!- FUNCTION: THE PEPLOMER PROTEIN MEDIATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Coronaviridae; Coronavirus.
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Mammalia; Eutheria; Ce
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Chaix J.C., Puigserver A., Guilloteau P.;
                                                                                                                                                                                                                                                                                                   TISSUE=Pancreas;
MEDLINE=98079203; PubMed=9418008;
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Last annotation update,
(EC 3.4.21.71).
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STANDARD; PRT; 475
AC O54161;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence updain
DT 16-OCT-2001 (Rel. 40, Last annotation upo
DE Alpha-L-arabinofuranosidase precursor (EG)
CO Alpha-L-arabinofuranosidase precursor (EG)
DE Alpha-L-arabinofuranosidase precursor (EG)
CO Alpha-L-arabinofuranosidase precursor (EG)
CO AREB OR SC7H1.02.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Act
OC Actinomycetales; Streptomycineae; Strepto
OX NCBI_TaxID-1902;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Murphy L., Harris D., Parkhill J., Barre:
RA Murphy L., Harris D., Parkhill J., Barre:
RA Submitted (JAN-1998) to the EMBL/GenBank,
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PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
Pfam; PF00089; trypsin; 1.
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InterPro; IPR001
InterPro; IPR001
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                                                                                                                                                                                                                                                                                                                                                  ALPDILQQGKLLVVDYATCSNPSWWGSTVKTNMICAGGD----GVTSSCNGDSGGP----
                                                                                                                                                                                                                                                                                                                                                                           GLPRRVQE----LSDVRT----SWTLTPITTGRWNAAYDIWESPVTNSGNGYSGGAELMI
                                                                                                                                                                                                                                                                                                                                                                                                       HEKWNSNQLAQGNDIALLKLASSVPLTDKIQLGCLPAAGTILPNNYVCYVTGWGRLQSNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRWDARDVAGGRYRVINNVWGAETAQCIE-----VG-----LETGNFTITRAD---
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57; Conservative
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243
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    to the EMBL/GenBank/DDBJ
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                                                                                                      Actinobacteria; Actinobacteridae;
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ACTIVATION PEPTIDE (BELASTASE 2.
CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (BY SIMILARITY.
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Pred.
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                                                                                     Streptomycetaceae;
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No. 1
                                                                                                                                                                           update)
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                                                                                                                                               update)
(EC 3.2.1.55) (Arabinosidase).
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    Rajandream databases.

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                   M.A.;
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RESULT 10
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Matches 43
                                                 Gregor J., Davis N.W., Kirkpatrick Mau B., Shao Y.;
                                                                                                                                                                                                                                                            YBFM_ECOLI P75733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
   SEQUENCE
                                                                      STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., R
                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
16-CCT-2001 (Rel. 40, Last annotation
Hypothetical protein ybfM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000772; Ricin_B_lectin.
Pfam; PF00652; Ricin_B_lectin; 1.
SMART; SM00458; RICIN; 1.
PROSITE; PS50231; RICIN_B_LECTIN; 1.
                                                                                                                                                                                   Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                                               Escherichia
                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                  YBFM OR B0681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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SUBCELLULAR LOCATION: Secreted.
SUBJEATIVE BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES
SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-arabinofuranoside residues in alpha-L-arabinosides.
                         complete genome sequence 
nce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                     PFIYRTSSDPT
                                                                                                                                                                                                                                                                                                                                                            NYIAYRRTTPT
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                                                                                                                                                                                                                                                                                                                                                                                                         SPVTNSGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGA-----TWEVWYADWDW
                                                                                                                                                                                                                                                                                                                                                                                                                                PPTDGTCALPSTY---RW----SSTGV-----LAQPKSGWVALKDFTTVTHNGRHLVYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---NNVAAYPAIYFGCHWGACTSNSGLPRRVQELSDVRTSW-TLTPITTGRWNAAYDIWF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WSCSGGANQQWRVNSDGTVVGVESGLCLEAAGAGTANGTAVQLWTCNGGGNQKWTGLTGT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WDARDVAGGRYRVINN--VWGAETAQCIE-VGLETGNFTITRADHDNG-------
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  FROM
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475 AA;
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   Z.A
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166 R
50045 MW;
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22.5%;
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Pred.
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                                     of Escherichia
                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                         subdivision;
                                                           H.A.,
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No. 4.1;
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                                                                                                                                                                                                                                                                          468
                                                                                                                                                                                                                       update)
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                                                            Goeden M.A., Rose
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                                                                          Rode
                                                                      Perna N.T., Buri
ode C.K., Mayhew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77;
                                     coli K-12.";
                                                                                                                                                                         Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Length 475;
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                                                                                    Burland
                                                             D.J.,
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RESULT 11
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ID GUXB_C
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AC P50899
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P50899;
01-OCT-1996
01-OCT-1996
01-OCT-1996
 SEQUENCE OF 54-75. MEDLINE=93209933;
                                   cellulolytic
Biochem. J. 3
                                                                                                                                                                         Cellulomonas fimi
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or-or-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Exoglucanase B precursor (EC 3.2.1.91) (Exocellobiohydrolase (1,4-beta-cellobiohydrolase B) (CBP120).
CBHB OR CENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000172; AAC73775.1; --
EMBL; D90707; BAA35329.1; ALT
ECOGene; EG13659; ybfm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"A 718-kb DNA sequence of the Escherichia

corresponding to the 12.7-28.0 min region

DNA Res. 3:137-155(1996).
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                                                                                                                                                                       STRAIN-ATCC 484;
MEDLINE-96003898; PubMed-7575482;
                                                                                                                                                                                                                                                                           Actinomycetales; Micrococcineae; NCBI_TaxID=1708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; SEQUENCE 468 AA; 5:
                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                     Shen H., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., "Cellobiohydrolase B, a second exo-cellobiohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97061202; PubMed=8905232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RADHDNGNNVAAYPAIYFGCHWGACTSNSGLPRRVQELSDVRTSWT-------
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                                                                      bacterium Cellulomonas
311:67-74(1995).
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PubMed=8458833
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954B5A778AE1C2E4 CRC64;
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InterPro; IPR003961; FN_III.
InterPro; IPR003962; FnIII_repeat.
InterPro; IPR000556; Glyco_hydro_48.
Pfam; PF00553; CBD_2; 1.
Pfam; PF00041; fn3; 3.
Pfam; PF00041; Glyco_hydro_48; 1.
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PRINTS; PR00844; GLHYDRLASE48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.; "Cellulose-binding polypeptides from Cellulomonas fimi: endoglucanase D (CenD), a family A beta-1,4-glucanase."; Bacteriol. 175:1910-1918(1993).
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
                                                                   Score 82.5; I
Pred. No. 12;
Pred. Mismatches
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Ol-FEB-1994 (Rel. 28, Created)
Ol-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Nucleotide sequence of the E2-peplomer protein gene and nucleotide sequence of the upstream polymerase gene of tr gas gastroenteritis virus (Miller strain).";
Adv. Exp. Med. Biol. 276:301-306(1990).
                                                                                                                                                   CARBOHYD
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Coronaviridae;
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FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE TO THE HOST CELL RECEPTOR AND IS INVOLVED AND IN SYNCYTIUM FORMATION.
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BY SIMILARITY.

EZ GLYCOPROTEIN.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

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                    InterPro; IPR001307; Rhodanese.
InterPro; IPR001763; Rhodanese_
                                                                                                                  the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-ATCC 13032;

MEDLINE-96337861; PubMed-8772169;

MEDLINE-96337861; PubMed-8772169;

Jaeger W., Peters-Wendisch P.G., Kalinowski J., Puehler A.;

Jaeger W., Peters-Wendisch P.G., Kalinowski J., Puehler A.;

ACOTYNEBACTETIUM Glutamicum gene encoding a two-domain protein similar to biotin carboxylasses and biotin-carboxyl-carrier protein arch. Microbiol. 166:76-82(1996).

-I- CATALYTIC ACTIVITY: Thiosulfate + cyanide - sulfite + thiocyanic - SIMILARITY: BELONGS TO THE RHODANESE FAMILY.
                                                             EMBL; U35023;
HSSP; P52197;
                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Corynebacterium.
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(Rel. 36, Last sequence update)
(Rel. 36, Last annotation update)
sulfurtransferase (EC 2.8.1.1) (Fragment).
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                                                                               AAB40889.1;
    01763; Rhodanese_domain
Rhodanese; 1.
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(POTENTIAL).
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Best Local Similarity
Matches 44; Conser
                                                                                                                                                                                                                    rucerPro; IPR002552; Corona_S1.
Pfam; PF01600; Corona_S1; 1.
Pfam; PF01601; Corona_S1; 1.
Glycoprofice
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VGL2_CVPPR
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ACT_SITE 1
SEQUENCE 22
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15-JUL-1999
                                                                                                                                                                                               Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Some or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92410651; PubMed-1326823; Sanchez C.M., Gebauer F., Sune C., "Genetic evolution and tropism of the state of the st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porcine transmissible gastroenteritis coronavirus (strain Viruses; ssRNA positive-strand viruses, no DNA stage; Nide Coronaviridae; Coronavirus.
                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                       EMBL; M94101; AAA47109.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Type I membrane protein.
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i01; Corona_S2; ...

in; Envelope protein; Transme...

1 16 BY SIMILARITY.

17 1447 E2 GLYCOPROTEIN.

17 1388 EXTRACELLULAR (POTENTIAL).

189 1408 POTENTIAL.

1409 1447 CYTOPLASMIC (POTENTIAL).

1409 1440 CYTOPLASMIC (POTENTIAL).

1409 1430 CYS-RICH.

1409 1430 RECEPTOR-BINDING (POTENTIAL).

N-C 465 N-LINKED (GLCNAC. ..) (PO
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(Rel. 28, Last sequence update)
(Rel. 38, Last annotation update)
tein precursor (Spike glycoprotein
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DOMAIN CARBOHYD

(POTENTIAL)

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VGL2_CVPPU
ID VGL2_CVPPU
ID VGL2_CVPPU
AC P07946;
DT 01-AUG-1988
DT 01-AUG-1988
DT 15-JUL-1999
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Best Local S
Matches 31
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Coronaviridae; Cor
NCBI_TaxID=11151;
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                                           SEQUENCE FROM N.A.

MEDILINE-87253116; PubMed-3037011;

Rasschaert D., Laude H.;

"The predicted primary structure of the peplomer porcine coronavirus transmissible gastroenteritis J. Gen. Virol. 68:1883-1890(1987).
      SEQUENCE FROM N.A MEDLINE-88129049;
                                                                                                                                                                                Porcine
                                                                                                                                                                                                                                                                                                                                                                                                184
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Similarity 24.6%;
31; Conservative
                                                                                                                                                    transmissible gastroenteritis coronavirus (strain Purdue); ssRNA positive-strand viruses, no DNA stage; Nidovirales iridae; Coronavirus.
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                                                                                                                                                                                                                    (Rel.
                                                                                                                                                                                                                                                                                                                                           249
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    precursor
                                                                                                                                                                                                  08, Created)
08, Last sequence update)
38, Last annotation update)
recursor (Spike glycoprotein)
        PubMed-2829461
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Spaan W.J.M.;
"The nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002552; Corona_S2.
Pfam; PF01600; Corona_S1; 1.
Pfam; PF01601; Corona_S2; 1.
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; A27106; VGIHE2.
; JS0336; VGIHE3.
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FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE B
TO THE HOST CELL RECEPTOR AND IS INVOLVED IN
AND IN SYNCYTIUM FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
      ; CAA29175.1; -.
; BAA00072.1; -.
; AAA47911.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   de sequence of the peplomer gene of porcine gastroenteritis virus (TGEV): comparison with the he peplomer protein of feline infectious peritonitis
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Matches 202;
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O1-JAN-1998 (TrEMBLrel. 0
O1-JAN-1998 (TrEMBLrel. 0
O1-DEC-2001 (TrEMBLrel. 1
CELLULASE (EC 3.2.1.4).
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MEDLINE-98242392; PubMed-9581291;
MEDLINE-98242392; PubMed-9581291;
MEDLINE-98242392; PubMed-9581291;
MEDLINE-98242392; PubMed-9581291;
MEDLINE-98242392; PubMed-9581291;
Medlidorsdottir S.H., Palsdottir A., Hrgyvidsson G.O.,
Mistylansson J.K., Holst O., Eggertsson G.;
MCloning, sequencing and overexpression of a Rhodothermus marinus gene encoding a thermostable cellulase of glycosyl hydrolase family 12.";
Appl. Microbiol. Biotechnol. 49:277-284(1998).
EMBL; U72637; AAB55594.1; -.
InterPro; IPR002594; Glyco_hydro_12.
Pfam; PF01670; Glyco_hydro_12; 1.
Probom; PD004316; Glyco_hydro_12; 1.
Probom; PD004316; Glyco_hydro_12; 1.
                                                                                                                                                                       Hydrolase; Glycosidase.
SEQUENCE 260 AA; 28770 MW; 94F197DB7D0D247A CRC64;
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Bacteria; CFB group;
NCBI_TaxID=29549;
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61 FGCHWGA-----CTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGN 114
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                                               ELCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVAAYPAIY 60
                               ELCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVAAYPAIY 99
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Rhodothermus group; Rhodothermus.
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OTILULASE (EC 3.2.1.4).
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Matches 89; Conserv
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"Cloning and expression of an endocellulase gene from a n Streptomycete isolated from an East African soda lake.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF33376; AAF91283.1; -.
HSSP; P07986; IEXG.
InterPro; IPR002594; Glyco_hydro_12.
InterPro; IPR001230; Prenyltn.
InterPro; IPR001230; Prenyltn.
Pfan; PF01670; Glyco_hydro_12; 1.
PFROM; PD004316; Glyco_hydro_12; 1.
PFROM; PD004316; Glyco_hydro_12; 1.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SEQUENCE 371 AA; 38481 MW; OE1BC4288A148914 CRC64;
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No. 3.9e-26;
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Best Local S
Matches 77
                                                                                                                                                                                                                                                                        008468;
008468;
01-JUL-1997
01-JUL-1997
01-DEC-2001
                                                                                                                                                                                                   Streptomyces halstedii.
Streptomyces halstedii.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Streptomycetaceae; St
                 InterPro;
InterPro;
                                         "Two genes encoding an endoglucanase are clustered and co-regulated by a T halstedil JMB.";
Biochem. J. 324:403-411(1997).
EMBL; U51222; AAC45429.1; -.
HSSP; P07986; 1EXG.
                                                                                                                                                                                                                                                  CELA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00553; CBD_2; 1.

Pfam; PF01670; Glyco_hydro_12; 1.

PrODom; PD004316; Glyco_hydro_12; 1.

PROSITE; PS00561; CBD_BACTERIAL; UNKNOWN_1.

Hydrolase; Glycosidase.

SEQUENCE 382 AA; 39398 MW; 21C014342EFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Streptomycineae; NCBI_TaxID=1928; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces rochei (Streptomyces parvullus).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                               Actinomycetales;
NCBI_TaxID=1944;
                                                                                                                                                                                                                                                                CEL2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 148:119-124(1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mastromei G.; "Characterization and sequence analysis of a
                                                                                                                       Santamaria-Sanchez R.I.;
                                                                                                                                   Garda-Salas A.L.,
                                                                                                                                              MEDLINE=97307849; PubMed=9182697;
                                                                                                                                                            STRAIN-JM8;
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001919; CBD_2.
InterPro; IPR002594; Glyco_hydro_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perito B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95011642; PubMed=7523249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  189
                                                                                                                                                                                                                                                                                                                                                                                                                                           165
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                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                           UL-1997 (TrEMBLrel. 04,
UL-1997 (TrEMBLrel. 04,
EC-2001 (TrEMBLrel. 19,
(EC 3.2.1.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGGYMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDLKAFIDDAVARG
                                                                                                                                                                                                                                                                                                                                                                                          LAGNDWYLTSIQAGFEPWQNGAGLAVNSFSSTV
                                                                                                                                                                                                                                                                                                                                                                                                       YIRPEWYLHAVETGFELWEGGAGLRSADFSVTV :||| ::: ||| |: |||| || || |||
                                                                                                                                                                                                                                                                                                                                                                                                                                          VGQIQPIGSQVGTASVAGRTWEVWSGGNGTNDVLSFVAPSAMSSWSFDVMDFVRATVARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPGTALPARISGISSAPSSISYGFVDNAVYNASYDIWLDPTPRTDG--VNRTEIMIWFNR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
  IPR001919; CBD_2.
IPR002594; Glyco_hydro_12
0553; CBD_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                   Fernandez-Abalos J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                   Created)
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Pred.
                                                                                                                                                                                                                                                                                                                            PRT;
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No. 2.
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                                                                                             codon
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.6e-22;
                                                                                             a cellulose-binding codon in Streptomyces
                                                                                                                                   Sanchez
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                                                                                                                                                                                                                                                                           update)
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Ruiz-Arribas

protein

Streptomyces.

Length 382

Indels

6

Gaps

4.

106 89

188

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SQUERRAL PROPERTY OF THE PROPE
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                                                                                                 "A set of ordered cosmids and a detailed genetic and pn the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).

EMBL; Al133210; CAB61599.1; -.

EMBL; Al133210; CAB61599.1; -.

R HSSP; P07986; IEXG.

R InterPro; IPR001919; CBD_2.

R InterPro; IPR002594; Glyco_hydro_12.

Pfam; PF00553; CBD_2; 1.

R Pfam; PF00553; CBD_2; 1.

R Pfam; PF01570; Glyco_hydro_12; 1.

R Pfam; PF01570; Glyco_hydro_12; 1.

R PROSITE; PS00561; CBD_BACTERIAL; UNKNOWN 1.

R PROSITE; PS00561; CBD_BACTERIAL; UNKNOWN 1.
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Best Local :
Query Match 28.0
Best Local Similarity 36.0
Matches 77; Conservative
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Q9RJY3;
Q9RJY3;
01-MAY-2000 (TIEMBLICEL: 13, C:
01-MAY-2000 (TIEMBLICEL: 13, Li
01-DEC-2001 (TIEMBLICEL: 19, Li
PUTATIVE SECRETED CELLULASE B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01670; Glyco_hydro_12; 1.
proDom; PD004316; Glyco_hydro_12;
Hydrolase; Glycosidase,
SEQUENCE 377 AA; 38829 MW; 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(4),
Cerdeno A.M., Parkhill J., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oliver K., Harris D.; Submitted (NOV-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-A3(2);
Oliver K., Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Redenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97000351; PubMed-8843436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                           Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCGRWDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVA--AYPAI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEIMIWLNKVGPIQPIGSQAGTASVGGRTWQVWRGSNGSNDVISFVAPSAVASWS-FDVM
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                         28.0%;
36.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barrell B.G., Rajandream M.A
e EMBL/GenBank/DDBJ databases
  31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
B.
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Score 345; DE
Pred. No. 1e-2
81; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
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Pred. No. 5.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                      1e-21;
                                                                                                                                                                                                                                                                                                                                                                                     genetic and
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  97;
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                                          Length 381;
                                                                                                                     CRC64;
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  Indels
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SIGNAL
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01-NOV-1996 (TrembLrel.
01-DEC-2001 (TrembLrel.
CELLULASE B PRECURSOR.
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InterPro; IPR002594; Glyco_hydro_12.
InterPro; IPR002594; Glyco_hydro_12.
InterPro; IPR00259; CBb_2; 1.
InterPro; IPR0053; CBb_2; 1.
InterPro; IPR0053; CBb_2; 1.
InterPro; IPR004316; Glyco_hydro_12; 1.
INTERPROSITE; PS00561; CBb_BACTERIAL; UNKNOWN_1.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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NCBI_TaxID=1916;
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IQPIGSPYGTASVGGRTWEVWSGGNGSNDVLSFVAPSAISGWSFDVMDFVRATVARGLAE
                                          VMPGGSRVATVELAGATWEVWYADWDWNYIAYRRTTPTTSVSELDLKAFIDDAVARGYIR 191
                                                                                          TDLPVRLDTVSAAPSSISYGFVDGAVYNASYDIWLDPTARTDG--VNQTEIMIWFNRVGP
                                                                                                                                          SGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWLNWNGG
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41
381 AA;
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Pred. No. 1.5e-21;
""matches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
CELLULASE B
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01-NOV-1999
01-NOV-1999
01-JUN-2001
CELLULASE.
 SEQUENCE
                                                                                                            O31030 PRELIMINARY; PRT; O31030; O1-JAN-1998 (TrEMBLrel. 05, Create O1-JAN-1998 (TrEMBLrel. 05, Last s 01-OCT-2001 (TrEMBLrel. 18, Last a BETA(1,4)-GLUCAN GLUCANOHYDROLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR001919; CBD_2.
Interpro; IPR002594; Glyco_hydro_12.
pfam; PF00553; CBD_2; 1.
pfam; PF01670; Glyco_hydro_12; 1.
proDom; PD004316; Glyco_hydro_12; 1.
SEQUENCE 384 AA; 40918 MW; D3968
                             Pectobacterium.
NCBI_TaxID-555;
                                                                  Bacteria;
                                                                              Pectobacterium carotovorum
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                    GRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVA--AYPAIYFGCHWGACTSN 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRYVVQNNRWGSSSPQCV-TATDIG-FRLIQADGSVPINGAPKSYPSVFNGCHYINCSPG 109
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FROM N.A
                                                               Proteobacteria; gamma
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ROLASE PRECURSOR.
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Pred. No. 1.1e-20;
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                                                                                carotovorum
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                                                                Enterobacteriaceae;
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Query Match
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Matches 68
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Bacteria; Firmicutes; Actinobacteria; Actinobacterroc

Bacteria; Firmicutes; Streptomycetaceae;
                            MEDLINE-97000351; PubMed-8843436; Redenbach M., Kieser H.M., Denapaite D., Kinashi H., Hopwood D.A.; Rinashi H., Hopwood D.A.; "A set of ordered cosmids and a detailed the 8 Mb Streptomyces coelicolor A3(2) chem Microbiol 21:77-96(1996).
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002594; Glyco_hydro_12
Pfam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1
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"Characterization of Erwinia carotovora subsp. carotovora LY34 endo-
"Character glucanase genes and rapid identification of their gene
                                                                                                                                                                                                                                                                  Murphy L., Submitted
                                                                                                                                                                                                                                                                                               STRAIN-A3(2);
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SIGNAL 1
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                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                       Submitted
                                                                                                                                                                                                       Cerdeno A.M.,
                                                                                                                                                                                                                  STRAIN-A3(2);
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98096373; PubMed-9434760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYTENSGLPIKLSSNKSITSNVTYSIKSTATLYAAYDVWFHTTDKASWDSTPTDELMIWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-TSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGGAELMIWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTNDVGQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWNGGVMPGGSRVATVELAGATWEVWYADW------DWNYIAYRRTTPTTSVSELDLKA
   PF01670;
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IPR002594; Glyco_hydro_12.
1670; Glyco_hydro_12; 1.
                                                                                                                                                                                     .M., Parkhill J., (MAY-2000) to th
                                                                                                                                                                                                                                                                  (MAY-2000)
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264 AA;
                                                                                                                                                                                                                                                                                 Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RKKWMSNAKYISSVELGTEIFGGDGQIDITKWSVDVK
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264 B
29634 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                          HYDROLASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                     Barrell B.G., Rajandream
EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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No. 4.1e-1
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                                                                                                                                                                                                                                                                                                                                                      Actinobacteridae; entomycetaceae; Streptomyces.
                                                              chromosome
                                                                             genetic and
                                                                                                          Eichner
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                                                                                                           Cullum
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                                                                                                           J.,
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Best Local
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060033;

01-NOV-1996 (TIEMBLIEL.

01-NOV-1996 (TIEMBLIEL.

01-JUN-2001 (TIEMBLIEL.
                                                                                                                               STRAIN-MSB8 / DSM 3109;

MEDITINE-99287316; PubMed-10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria

genome sequence of Thermotoga maritima.";

Nature 399:333-329(1999)

Nature 399:333-329(1991).
                         InterPro; IPR002594; Glyco_hydro_12.
Pfam; PF01670; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
Signal; Hydrolase; Glycosidase; Complete
SIGNAL 1 1 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MSB8 (DSM3109);
MEDLINE=96425879; PubMed=8828221;
Liebl W., Ruile P., Bronnenmeier K., Riedel K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENDO-1,4-BETA-GLUCANASE PRECURSOR (EC 3.2.1.4) (CELLULASE)
(ENDOCLUCANASE) (CARBOXYMETHYL CELLULASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD004316; Glyco_hydro_12;
Hydrolase.
SEQUENCE 244 AA; 26123 MW; 2C/
                                                                                                                                                                                                                                                                                                                                                                            "Analysis of a Thermotoga thermostable cellulases, C
                                                                                                                                                                                                                                                                                                                                                                                                               Greif I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotoga maritima.
Bacteria; Thermotogales;
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                                                                                                      EMBL; AE001800; AAD36592.1; TIGR; TM1525; -.
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              recombinant enzymes.";
Microbiology 142:2532-2542(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGRWDARDVAGGRYRVINNVWGAET-AQCI--EVGLETGNFTITRADHDNGNNVAAYPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKAFIDDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILKWIKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AELMIWLNWNGGVMPGGSRVATVELAGATWEVWYADWDWNYI-AYRRTTPTTS--VSELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YFGCHWGACTSNSGLPRRVQELSDVRTSWTLTPITTGRWNAAYDIWFSPVTNSGNGYSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDQWGNTSLNG--YTLYNNIWGSGAGSQCVWANSGTDWGVW----ADHPNTDGIKSYP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -EIMLWVNHHGAVGPLGTFQGSVGLGGHTWDVYKGNNGANEVFSFLRTSDSNSGTVNILP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----NAKKVINKPITSLSSLTSSYNVTVPSSGAYNTSYDIW-----DTDYDY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TKGWMGNE-TIGDVQFGYEITSSAGGLDFRTNNLTV
Ă,
31734 MW;
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26.7%;
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                                                                                                                                                                                                                                                                                                                                                                              CelA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotoga
                                                                                                                                                                                                                                                                                                                                                                           maritima DNA fragment encoding two similar CelA and CelB, and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Pred. No. 6.
ENDO-1,4-BETA-GLUCANASE.
72C0A5ACAD7BA358 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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WDARDVAGGRYRVINNVWGAETAQCIEVGLETGNFTITRADHDNGNNVAAYPAIYFGCH-

Query Match Best Local Matches

67;

Conservative

43;

Score 196.5; Pred. No. 3.8e 3; Mismatches

.8e-09; DВ

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Length

Indels

57;

Gaps 64

15;

Similarity

15.9%; 26.7%;

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P965UL7
P965UL
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Best Local S
Matches 70
P96492 PRELIMINARY; PRT; 274 AA.
P96492; Ol-MAY-1997 (TrEMBLrel. 03, Created)
Ol-JAN-1998 (TrEMBLrel. 05, Last sequence update)
Ol-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENDO-1,4-BETA-GLUCANASE B (EC 3.2.1.4) (CELLULASE) (ENDOGLUCANASE)
                                                                                                                                                                                                                                                                                                         STRAIN=22706-MC24;
MEDLINE=93356813; PubMed=8352795;
Dakhova O., Kurepina N., Zverlov V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Bok J.D., Eveleigh D.
Submitted (JUN-1997)
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-137 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zverlov V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Z2706-MC24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermotoga neapolitana
                                                                                                                                                                                                                                                                                          Velikodvorskaya G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-137 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
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No. 1.7e-09;
                                                                                                                                                                                                                                                                                                                Svetlichnyi V.,
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A COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Evelin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Nutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
T "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
L Nature 393:537-544(1998).
R Tuberculis; Rv1090; T.
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Best Local Similarity
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O1-JUN-1998 (TEMBLrel. 06, Created)
O1-JUN-1998 (TEMBLrel. 06, Last sequence update)
O1-DEC-2001 (TremBLrel. 19, Last annotation update)
HYPOTHETICAL 16.4 KDA PROTEIN.
RV1090 OR MTV017.43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002594; Glyco_hydro_12.
PfAm; PF01570; Glyco_hydro_12; 1.
ProDom; PD004316; Glyco_hydro_12; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 151 AA; 16404 MW; 8BCC10CFFC9C8E54 CRC64;
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                                                                  YIRPEWYLHAVETGFELWEGGAGLRSADFSVTV 221
                                                                                                                                                                                                                                                         TNLPTEVGQILSAPTSIDYNYPTTGVWDASYDICLDSTPKTTGVN----QQEIMIWFNHQ
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PITDSWYLTSIRAGLEPWSDGVGLGVDSFSAKV
                                                                                                                                 GSIQPVGSPVGNTTIEGKNFVVWDGSNGMNNAMAYVATEP-IEVWSFDVMSFVDHTATME
                                                                                                                                                                                          GGVMPGGSRVATVELAGATWEVWYADWDW-NYIAYRRTTPTTSVSELDLKAFIDDAVARG 188
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                                                                                                                                                                                                                                                                                                                                                                                                              15.7%; Score 194; DB 1: 33.3%; Pred. No. 3e-09;
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Best Local S
Matches 63
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O94218;
O1-MAY-1999 (TrEMBLrel. 10, C)
O1-MAY-1999 (TrEMBLrel. 10, L)
O1-DEC-2001 (TrEMBLrel. 19, L)
XYLOGLUÇAN-SPECIFIC ENDO-BETA
                                                                                                                                                                  000095;
000095;
01-JUL-1997
01-JUL-1997
01-DEC-2001
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A xyloglucan-specific endo-beta-1,4-glucanase from A xyloglucan-specific endo-beta-1,4-glucanase from A culeatus: expression cloning in yeast, purification characterization of the recombinant enzyme.";
Glycobiology 9:93-100(1999).
EMBL; AF043595; AAD02275.1;
InterPro; IPR002594; Glyco_hydro_12.
Pfam; PF01670; Glyco_hydro_12; 1.
                  Hypocreales; Hypocreaceae;
NCBI_TaxID=51453;
                                                                  Trichoderma reesei (Hypocrea jecorina).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                                                                                                                          01-JUL-1997 (TrembLrel.
01-JUL-1997 (TrembLrel.
01-DEC-2001 (TrembLrel.
ENDO-BETA-1,4-GLUCANASE
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SIGNAL
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ProDom; PD004316; Glyco_hydro_12; 1.
Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-KSM 510;
MEDLINE=99102417; PubMed=9884411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pauly M., Andersen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                               SEYSISIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ADFSVTVQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WDWNYIAYRTTPTTSVSELDLKAFIDDAVARGYIRPEWYLHAVETGFELWEG-GAGLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238
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                                                                                                                                                                                                                                                                      PRELIMINARY;
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rel. 19, Last annotation update)
ENDO-BETA-1,4-GLUCANASE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25158 MW;
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                                              Hypocrea
                                                                                                                                          Last sequence up Last annotation 3.2.1.4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 178.5;
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XYLOGLUCAN-SPECIFIC ENDO-BETA-1,4-
GLUCANASE.
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                                                                     Sordariomycetes;
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ID O13454
AC O13454
DT O1-7AN
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DT O1-DEC
DE ENDO-1
GN CELA.
OS ASPERG
OC EUTO-1
GN CELAI
OX NCBL_T
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RP SEQUEN
RA KITANO
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                                                                                                      Query Match
Best Local S
Matches 63
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Best Local Similarity 28.6%; Pred. No. 1.6e-07;
Matches 68; Conservative 34; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O13454 PRELIMINARY;
O13454;
O1-5454;
O1-748-1998 (Tremblrel. 05, C:
O1-748-1998 (Tremblrel. 19, L:
O1-DEC-2001 (Tremblrel. 19, L:
ENDO-1,4-BETA-GLUCANASE (EC 3)
                                                                                                                                                                                                                                                                              TSukagoshi N.;

"Molecular cloning, purification and characterization of two endo-1,4-beta-glucanases from Aspergillus oryzae KBN616.";

Appl. Microbiol. Biotechnol. 46:538-544(1996).

EMBL; D83731; BAA22588.1; -

EMBL; D83731; BAA22588.1; -

InterPro; IPR002594; Glyco_hydro_12.

Pfam; PF01670; Glyco_hydro_12; 1.

ProDom; PD004316; Glyco_hydro_12; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
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pfam; pF01670; Glyco_hydro_12; 1.
proDom; pD004316; Glyco_hydro_12; 1.
Hydrolase; Glycosidase.
SEQUENCE 234 AA; 25159 MW; DF476EEDE384ADD1 CRC64;
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EMBL; AB003694; BAA20140.1;
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Kumagai H., Morikawa Y.;
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STRAIN-QM9414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97161783; PubMed-9008887;
Kitamoto N., Go M., Shibayama T., Kimura T., Kito Y.,
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                                                                                                                                     Local Similarity
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ELCGRWDARDVAGGRYRVINNVWGAET---AQCIEVGLETGNFTITRADHDNGNNVAAYP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTTSVSELDLKAFI----DDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTV 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY----ADWDWNYIAYRRTT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQ-----NSQIAIPQKRTVNSISSMFTTASWSYSG-SNIRANVAYDL-FTAANP 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YPAIYFGCHWGACTSNSGLP--RRVQELSDVRT--SWTLTPITTGRWNAAYDIWFSPVTN 111
                                                                                                                                                                                                                                                     Glycosidase.
239 AA; 26(
                                                                                                      Conservative
                                                                                                                                                                                                                                                  26096 MW; COF850E5DFEB455D CRC64;
                                                                                                14.0%; Score 172.5; DB 3
27.3%; Pred. No. 3.6e-07;
tive 37; Mismatches 86
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3.2.1.4).
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                                                                                                                                                              DB 3;
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                                    160 YIAYRRTTPTTSVSELDLKAFIDDAVAR-GYIRPEWYLHAVETGFELWEGG 209
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                                                                                                               WFSPVTNSGNGYSGGAELMIWLNWNGGVMPGGSRVATVELAGATWEVWY-----ADWDWN 159
TYSFVSATPINTFGG-DIKKFFDYITSKHSFPASAQYLINMQFGTEPFTGG
                                                                               -FTAADQNHYTYSGDYELMIWLARYGTIQPIGTQIDTATYEGHTWELWYGTTIQAGAEQK 175
                                                                                                                                                                AWHTTWTWNGGEGSVKSYSNSAVTFDKKLVSDVQSIPTDVEWSQDNTNVNA---DVAYDL
                                                                                                                                                                                                      AIYFGCHW------GACTSNSGLPRRVQEL-SDVRTSWTLTPITTGRWNAAYDI 104
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Search completed: August 15, 2002, 10:57:39 Job time: 393 sec

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Result
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Maximum
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Sequence 3 from Patent WO0196382.
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Thermostable cellulase Patent: WO 0196382-A 3 20-DEC-2001;
Prokaria ehf. (IS)
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AUTHORS Wicher, K.B., Holst, O.P., Hachem, M.Y., Karlsson, E.M. and
Hregytidsson, G.O.

TITLE Thermostable cellulase
JOURNAL Patent: WO 0196382-A 1 20-DEC-2001;
Prokaria ehf. (IS)

FEATURES Location/Qualifiers
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Submitted (25-SEP-1996) Department of
Institution of Biology, Grensasvegur
Location/Qualifiers
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1 (bases 1 to 1874)

Halldorsdottir,S., Thorolfsdottir,E.T., Spilliaert,R.,

Johansson,M., Thorbjarnardottir,S.H., Palsdottir,A.,

Hreggvidsson,G.O., Kristjansson,J.K., Holst,O. and Eggertsson,G.

Cloning, sequencing and overexpression of a Rhodothermus marinus
gene encoding a thermostable cellulase of glycosyl hydrolase family
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                                                                                                                                l (bases 1 to 1116) van Solingen,P., Meijer,D., van der Kleij,W.A.H., Barnett,C.C., Bolle,R., Power,S.D. and Jones,B.E. Cloning and expression of an endocellulase gene from a novel Streptomycete isolated from an East African soda lake
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Streptomyces sp. 11AG8 cellulase 12A (cel12A)
AF233376
AF233376.1 GI:9651812
Direct Submission
Submitted (10-FEB-2000) Microbial
International B.V., Archimedesweg
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van Solingen,P., Meijer,D., van G
Bolle,R., Power,S.D. and Jones,B
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Streptomyces sp. 11AG8
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                 CCAACGGGGTGAACCGGACCGAGATCATGATCTGGTTCAACCGGGTCGGCCCGGTCCAGC
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/note="Region: linker region"
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QDRYVYQNNRWGTSATQCINVTGNGFEEITQADGSVPTWGAPKSYPSVLDGCHYGNCAP
RTTLPMRISSIGSAPSSYRYTGNGVEITADDTULDPTRHGVNRTEIMIFFNWY
PVQPIGSPVGTAHVGGRSWEIVTGSNGSNDVISFLAPSAISSWSFDVKDFEVDQAVSHG
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PGGFTVDTTITNTGSTPVDGWELDFTLPAGHTVTSVWNALISPASGAVTARSTGSNGR
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/db_xref="GI:9651813"
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Sequence 2 from patent US 6187577.

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ORGANISM
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Matches 347; Conserv
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acggctacagcggcgcgagctgatgatctggctgaactggaacggcgcgcgtgatgc
                                                                                                                                           AGTCCTATCCCTCGGTCTACGACGGCTGCCACTACGGCAACTGCGCGCCCCGCACGACGC
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                                     GCAACGGCGTCTACAACGCCGCGTACGACATCTGG-----CTGGACCCCGACACCCCGCA
                                                                                        TGCCCATGCGGATCAGCTCGATCGGCAGCGCCCCAGCAGTGTCTCCTACCGCTACACCG
                                                                                                                                                                                               CCGGCAACGGTTTCGAGATCACCCAGGCCGACGGTTCGGTGCCGACCAACGGCGCCCCGA
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Sequence 2 1
AR168360
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Jones, B.E., Van Der Kleij, W.A.H., Van Solingen, P. and
Cellulase producing actinomycetes, cellulase produced
method of producing same
Patent: US 6287839-A 2 11-SEP-2001;
Location/Qualifiers
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patent US 6287839.
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Pred. No. 3.4e-10;
0; Mismatches 332;
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Best Local Similarity

Matches 269; Conserv
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                                                                                         GCAACGGTTCGAACGACGTGATCTCCTTCCTGGCGCCCTCCGCGATCAGCAGCTGGAGCT 1064
                   TCGGTTCGCCGGTCGGCACGGCCACGTCGGCCGCCAGCTGGGAGGTGTGGACCGGCA
                                                                                                                                                                                   CCATGCGGATCAGCTCGATCGGCAGCGCCCCAGCAGTGTCTCCTACCGCTACACCGGCA
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Unknown.
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Sequence
AR168362
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1 (bases 1 to 1716)

1 (bases 2 to 1716)

Jones, B.E., Van Der Kleij, W.A.H., Van Solingen, P. and Cellulase producing actinomycetes, cellulase produced method of producing same patent: US 6287839-A 4 11-SEP-2001;
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611 c 559 g
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patent US 6287839
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Pred. No. 1.7e-06;
0; Mismatches 227;
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Submitted (13-MAR-1996) Ramon I. Santamaria-Sanchez, Instituto Submitted (13-MAR-1996) Ramon I. Santamaria-Sanchez, Instituto Microbiologia Bioquimica, Consejo Superior de Investigaciones Cientificas / Universidad de Salamanca, Avda. del Campo Charro, s/n, Salamanca, Salamanca 37007, Spain
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Streptomyces halsted11
Streptomyces halsted11
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Streptomycetaceae; St
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Streptomyces
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NTIARGMAQNNWYLTSVQAGFEPWQNGAGLAVNSFSSTVNLGTPGTGSPGAPGEPVTA
CEVAYATNVWSDGFTADVTVANTGSTPVDSWRLSFTLPSGQRVTNAWNATVSGPTGAV
                                                                                                                                                                                                                                   /translation="mralphgprtprsligalilalatvaavlaaapaahadtivceo
YGSTTIQGRYVVQNNRWGASAPQCVTATDSGFRVTQADGAVFTNGAPKSYPSVFNGCH
YTNCSPGTNLPAQVSGIASAPSSISYGFVGSAYYNASYDIWLDETPKKNGVNRTEIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene=
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595. .1728
/translation="margkrllvSltavFatllgGIaLtlfGQGnaQahgvTmtpgSr
TYLCWLDAKTSTGSLDPTNPACKAALSESGSNALYNWFAVLDSNAGGRGAGYVPDGKL
                                                                                                                                                                   TATGLAHSAQVAAGASQTFGFQGTYSGTFSKPSGFSLNGARCA'
                                                                                                                          /note="cellulose binding
                                                                                                                                                                                                                                                                                             /protein_id="AAC45429.1"
/db_xref="GI:2209260"
                                                                                                                                                                                                                                                                                                                                                                                                        /gene-"celA2"
/EC_number-"3.2.1.4"
                                     /protein_id="AAC45430.1"
/db_xref="GI:2209261"
                                                                       /product-"p40"
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                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                 /product-"Cel2"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                     /note="beta-1,4-endoglucanase"
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halstedii beta-1,4-endoglucanase (celA2) gene,
, and cellulose binding protein (p40) gene, complete
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DEFINITION
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REFERENCE

cellulase; eglS gene; endoglucanase Streptomyces rochel. Streptomyces rochel Bacteria; Firmicutes; Actinobacteria Actinomycetales; Streptomycineae; S' 1 (bases 1 to 1470) Mastromei,G.

endoglucanase.

Actinobacteria; Actinobacteridae;

AUTHORS TITLE

JOURNAL

Direct Sub Submitted

Submission

(07-JUL-1993)

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                                                                                                                 GGTGAACTCCTTCTCCTCAACCGTGAA 1367
                                                                                                                                                                        CTGGTATCTCACCAGTGTCCAGGCAGGATTCGAGCCGTGGCAGAACGGTGCCGGACTCGC
                                                                                                                                                                                                                              GAGCTTCGACGTCATGGACTTCGTCCGGAACACCATCGCCCGCGGCATGGCGCAGAACAA
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SREGLS
S.rochei eglS gene.
X73953
X73953.1 GI:393391
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TELGWIDLLELIETVTNMPPOTGSPGTDGGHYTWNLDLPSGRSGDAVMFIQWVRSDSQEN
FFSCSDVVFDGGNGEVTGIRGSGSTPDDTPTPTPDPDFTFTDPHSGCMAVYRVTNYWS
GGFQGSVEVMNHSTTARDGWAVKWTPGAKAKVSSVWNGALTTGSDGAVTVRSLDYNRS
IPPDGSVTFGFTATSTGNNLPVGSIGCVNP"
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             cgatcacgacgggccgctggaatgccgcctacgacatctggttcagtcccgtcacgaatt 453
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                                                                           cgggattgccgcgcgcgtgcaggagctgtccgacgtgcgcacgagctggacgctcacgc
                                                                                                                   CGCCGAAGTCGTACCCGTCGGTCTTCAACGGCTGTCACTACACGAACTGTTCGCCGGGCA 493
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                                                                                                                                                                                                                                                              ccggggggcgctaccgggtgatcaacaacgtatggggcgcggagaccgcccagtgcattg 211
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                                                          CCGCGCTCCCCGCGGATCAGCGGCATCTCCTCCGCGCCCAGCAGCATCTCGTACGGCT
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327; Conserv
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Characterization and sequence
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Gene 148 (1), 119-124 (1994)
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1351: .1403
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/translation="MprurheprylraysaalltalallalltatapaQadtticee
FGSTV1OGRYVYQONNRGGTSATQCVTATDSGFRVTQADGSVPTNGAPKSYPSVENGCH
YTNCSPGTALPARISGISSAPSSISYGFVDNAVYNASYDIWLDPTPRTDGVNRTEIMI
WFNRVGQIOPIGSQVGTASVAGRTWEVWSGGNCTNDVLSEVAPSAMSSWSEDVMDEVR
ATVARGLAGNDWYLTSIQAGFEPWQNGAGLAVNSFSSTVNTGGSQNPGDPNGPGDPGT
PAACTVSYATNWPGGFTANVTVTNNGSAPVDGWRLAFTLPSGQSVVHAMNASVSPSS
GAVTATGPAESARIAAGGSQSFGFQGAYSGSFAQPAAFQLNGTACSTV"
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/db_xref="GI:393392"
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/EC_number="3.2.1.4"
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Pred. No. 4.5e-05;
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Ramachandran, S. and
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Direct Submission
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Prairies, Laval, Quebec H7N 4Z3,
3 (bases 1 to 1565)
Shareck, F.
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WSPDVMDFVRETVARGKAQNDWYLTSVQAGFEPWQNGAGLAVNSFSSSTVTGGGTPGG
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Submitted (02-0CT-1997) Institut Armand Frappi
Prairies, Laval, Quebec H7N 423, Canada
Sequence update by submitter
On Oct 2, 1997 this sequence version replaced
Location/Qualifiers
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/function="hydrolase"
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/strain="66"
/db_xref="taxon:1916"
/clone="IAF12"
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Pred. No. 0.00077;
0; Mismatches 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23 NOV-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBLO 1SA E-mail: barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
Notes:
Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acyl-CoA dehydrogenase; aldehyde dehydrogenase; amidase; dihydroxy-acid dehydratase; DNA polymerase III beta Chain; export protein; gntR-famly transcriptional regulator; lacI-family transcriptional regulator; marR-family transcriptional regulator; coxidoreductase; reductase; regulatory protein; secreted cellulase precursor; secreted cellulose binding protein; tetR-family transcriptional regulator; transcriptional regulator; xylose repressor; xylose knase.
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Streptomyces coelicolor cosmid G
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A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                      Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot
                                                                                                                                               The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
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                                            program of Bibb et al., Gene 30:157-66(1984) as
                                                                                                                                                                                                                                                                                                                                                  (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (compl
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Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
  http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl.
                                                                                                                                                                                                                                                                                                                               strand).
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  CAUTION:
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correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bb before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
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/protein_id="CAB61582.1"
/protein_id="CAB61582.1"
/protein_id="CAB61582.1"
/db_xref="G1:6468422"
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/translation="DPROWWDALGEALSOCGEAVEAAVSVGGOOHGLVTLDARGEP
/translation="DPROWWDALGEALSOCGEAVEAVSVGGOOHGLVTLDARGEP
/TRALLWNDVRSAPQARRLIDEGGTANGVGGTGWAASGTEAVDEELLARVALDPALLPAV
VRPAGEVAGTVRDGHGLPFSKGTLVAAGTGDNAAAALGLGLRPGVPVMSLGTSGTAYAV
VRPAGEVAGTVRDGHGLPFSKGTLVAAGTGDNAAAALGLGLRPGVPVMSLGTSGTAYAV
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874. .936
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PFLDGERTPNLPHSSGLLHGLRHDTTAGQLLQAAYDGAVHSLLGALDLVLDADADPSA
PLLLIGGGARGTAWQQTVRRLSGRPVQIPEARELVALGAAAQAAGLLTGEDAAAVARR
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                                                                                                                                                                                          overlap. Contains match to Pfam entry PF00480 ROK, family and a possible helix-turn-helix motif at reads. .64 (+3.15 SD)"
                                                                                                                                                                                                                                                                                                                                                                xylose repressor xylR, 384 aa; fasta scores: opt: 2-score: 642.4 E(): 2-le-28; 29.4% identity in 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Pfam match to entry PF00370 FGGY, FGGY family carbohydrate kinases, score 514.30, E-value 8.7e-151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WNTAAGPVLDAVERDEATLNRITGVLSDAAPLLERDAASR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family of carbohydrate kinases signature and PS00445 FGGY family of carbohydrate kinases signature 2"
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/strain="A3(2)"
                                                     transl_table=11
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/product="putative xylose repressor"
                                                                                                                                    /codon_start=1
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Query Match
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3821, .5080
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/note="SCG11A.03, probable amidase, len: 201 aa; similar /note="SCG11A.03, probable amidase, len: 201 aa; similar to SW:AMPD_ECOLI (EMBL:X15237) Escherichia coli anhydro-N-acetylmuramy1-tripeptide amidase AmpD, 183aa; fasta scores: opt: 211 z-score: 267.1 E(): 1.7e-07; 39.5% identity in 114 aa overlap and to Streptomyces coelicolor SC2A11.21c; fasta scores: opt: 674 z-score: 751.6 E(): 0; 50.0% identity in 202 aa overlap. Contains match to Pfam entry PF01510 Amidase_2, N-acetylmuramoy1-L-alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MTDAWLALEPGADPVERARALRRAHETETEAGTVRRPVRAVVAD
SWRRSVRAGVGPDGTASVELMDGDLGAYRAEHPLSRVMPLVRELLGTFAADGEHLLAV
CDAHGRLLMVEGHPATERRAGENNEVPGARWSESAVGTNAPGTAVAVGRPVQVFAAEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SCG11A.04"
/note="SCG11A.04, possible transcriptional regulator, len:
aa; similar to TR:031551 (EMBL:Z99108) Bacillus subtilis
transcriptional regulator AcoR, 605 aa; fasta scores: opt:
393 z-score: 446.5 E(): 1.7e-17; 34.7% identity in 199 aa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to entry PF01510 Amidase_2,
N-acetylmuramoy1-L-alanine amidase, score 89.80,
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Saewipastswysrssrptaypydfyvyhytgefyaptlsifrdpekqysahyyvrss
DghyaQcyrefdiawhagnwdywrstgciehegworpepyfnwayeqsarltaaict
aygipkdrthiiahheypgsdhtdpgpfwdwtryirlvnfa"
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3041. .3646
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/note="Pfam match to
131.80, E-value 4e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative transcriptional regulator"
/protein_id="CAB61585.1"
/db_xref="GI:6468425"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      overlap
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/product="putative amidase"
/protein_id="CAB61584.1"
/db_xref="GI:6468424"
                                                                                                                                                                                                                                                                                                                       AAYAGPLLPGSQAPAVGRLRRRLADGLRAALIACGDPDLLADWAHAPWGEDDLDVWRA
                                                                                                                                                                                                                                                                                                                                                    YEDETVPPVTLRAELARLRGILGPGRLASRPYRLTMPVESDTSVVERRLRAGAVTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                  FIRRVQPWTCAAAPVHDPRTGRVLGAVDITGGDGLAHPHSLGFVQAVARAAESQLALL
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/db_xref="GI:6468423"
                                                                                          /note="SCG11A.05, thcA, aldehyde dehydrogenase,
                                                                                                                                                                                                                                                                                             LAAVRPTAATSSRLAALESELAAPNPW"
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                                                                highly similar
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      87.6;
                                                             to SW:THCA_RHOSN
DB
Length 41782;
                                                                (EMBL:U17129)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCTTCGACGTCATGGACTTCGTCCGGGCGACCGTCGCGCGGGACTCGCCGAGAACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgccgactgggactggaattacatcgcctaccggcgcacgacgcccaccacgtcggtgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCCATCGGCTCACCGGTGGGCACGGCCTCCGTCGGCGGCCGGACCTGGGAGGTGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGACGGCGCCGTCTACAACGCCTCGTACGACATATGG-----CTGGACCCGACGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cacgacgggccgctggaatgccgcctacgacatctggttcagtcccgtcacgaattccgg 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggccgcctatccggccatctacttcgggtgccactggggcgcctgcacgagcaattcggg 335
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11016950
2 /h-
                                                                                   Ng,W.V., Kennedy,S.P., Mahairas,G.G., Berquist,B., Pan,M., Shukla,H.D., Lasky,S.R., Baliga,N., Thorsson,V., Sbrogna,J., Swartzell,S., Weitr,D., Hall,J., Dahl,T.A., Welti,R., Goo,Y.A., Leithauser,B., Keller,K., Cruz,R., Danson,M.J., Hough,D.W., Maddocks,D.G., Jablonski,P.E., Krebs,M.P., Angevine,C.M., Dale,H., Isenbarger,T.A., Peck,R.F., Pohlschrod,M., Spudich,J.L., Jung,K.-H., Alam,M., Freitas,T., Hou,S., Daniels,C.J., Dennis,P.P., Omer,A.D., Ebhardt,H., Lowe,T.M., Liang,P., Riley,M., Hood,L. and
                                                                                                                                                                                                                                                                                                                                   11202 bp
Halobacterium sp. NRC-1 section
AE005123 AE004437
AE005123.1 GI:10581826
                                                 DasSarma, S. From the cover: genome
                                                                                                                                                                                                                                                                      Halobacterium sp. NRC-1
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                     Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                       Halobacterium sp. NRC-1.
 (bases
                                                                                                                                                                                                                                   (bases 1 to 11202)
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                                   Natl. Acad.
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                                    sequence of halobacterium species NRC-1 USA 97 (22), 12176-12181 (2000)
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                                                                                                           Dennis, P.P.,
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FEATURES
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BASE COUNT
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                                                                                                                                                                                                                                                               99ccggggccacctgggaagtctggtatgccgactgggactggaattacatcgcctaccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACCTGCGTCGCGCGCGCGGATTTCCTCACGATCCACGTCCCCACTCACCGACGAGACCGA 7177
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CGACGTCACGTACCAGGGCGAGGTCGCCGACGAGGACGTCGCACTCGTCACGGCGGCCGC
                                                                                                                                                                                                    CCTCGCGGAGACCGCCGCACCGTCGCCGCGGCGCTTTCGACCCCCGCATCGAGCGCGT
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/product="threonine synthase"
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/product="filiosial834"
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RRSLAVRDTAARLLSGTQFRWILVAYTLYAFTWQAIAAFLPTFFTDGKEFAPVVGTVA
FGALFAVGAIAKPTAGTLSDTISRRALAVGALVLGAAALSAVVVVPSPVAAVGAVVVF
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FWGLVGALIVAAVIIARVT"
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TLLVTGLGMASGGFVVLATARSYAALLVGAAIVGTGAGLYPTAARALVADLYSTKQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(9890. .11137)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 4262)
Steiner,B., Meyer,R., Bowen,M. and Morrill,W.
Random sequencing of Burkholderia pseudomallei strain
clinical PCR development
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Bacteria; Proteobacteria; beta subdivision;
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                                                                                              GYFRKGEGTAPGLICFEYHVCVASMVLLLVADDAYCFAVAMETLTLSARTFLVARINHRI
ABITRAAFVYFLISHVGALALLLCFGLLAGTGDYTFANMRIQHLDGLAASAAFVLAL
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FFGTVFLGRPREAKLERARDASPWERIAFGWFAAASVLLGLAPVQYVKVLDALTRALY
SCGNPFVTARMQDTAEGFGQPIREIFTPFFRIERQLPSPFDRQPAYRMSVADRTWHLL
YEPIAALANRVAALVGRLQTGRIAIYLTYSFIVLIALLTVVRRW"
1 1502 c 1477 g 538 t 1 others
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Qpyrmlhklfnkesvvagareplfrgapyvvmaamalacaivptlstelpfspaadai
Alvglfalarvalslaamdigtafgtlgarremligflaepallmvlfsaslitrstl
LTSIVAALGHRELAIVPSLAFAGIAFTLVSLAENARLPVDNPATHLELTMIHEALILE
                                                                          GAGTAGTNHGWLLFAPVSTARASYMPALEMLFEVACCALAWLLVRRFYHGRLRRAAPW
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                                                                                                                                                                                                                                                                                        /product="hydrogenase-4 component B"
/protein_id="AAK06855.1"
/db_xref="Gi:12744949"
/translation="MEQGLLLRCVLEYALAWLALGCAGLANLRRTGVIAHGLEPLGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="formate hydrogenlyase subunit
/protein_id="AAK06856.1"
/db_xref="GI:12744950"
                                                                                                                                                                                                                                                                         AGLVLAALGLAGVFAGPSSAVLPLGLPDLPFHLRVDPLSAYFLFVLGVVTÅGVGAFSS
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/strain="G9313"
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LRAYAHWARRTGDPLARRVAAQTARFLLDELGSKAPADMFTSSLD TPVQLTEVLGGDDGRWAAEVFGVTEAGTFEHGTSVLQLPADPDDA			gene
VALITGOGWPMTCFLIFNGRFFFCGTYYPKAAFLOLLSALSEIWR AAELRSMASGLBGGFPGAPELCDAVAGVLREQDTAHGGFGAP HYERTRASALSHAVARTGNAWARGGTVDOLGGGRARYSVACAL		/organism="Mycobacterium tuberculosis CDC1551" /strain="CDC1551" /db xref="taxon:83331"	
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	CDS		AUTHORS
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VTTRVECSKYFSQRDDALRAHATQIDPNAEFFAAPLAWQERLWPT			KEYWORDS
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))	208; Conservative 0; Mismatches 232; Indels 0; Gaps 0;	Matches

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EVPSYLRLP"
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LPGSVVKVYYNGDKSD
TVPNGSTVSVTLVSAE
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                                                                                                                                                                                                                                               gccggggccacctgggaagtctggtatgccgactgggactgggaattacatcgcctaccgg 609
                                                                                                                                                                                                                                                                                                                    tggctgaactggaacggcggcgtgatgccggggcggcagccgcgtggccaccgtggaacttg
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

24-JUN-1998; 19-NOV-1997; 19-NOV-1997;

98US-0104308. 97US-0974041. 97US-0974042.

Jones BE,

Van Der Kleij WAH,

Van Sollingen P,

Weyler W;

(GEMV) GENENCOR INT INC

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H. virescens inorg	Recombinant cosmid	Nucleotide sequenc	S. venezuelae pik	S. venezuelae pik	Sequence encoding	S. venezuelae macr	L05390 cDNA clone.	Mouse Sox1 cDNA.	Non-reducing sacch	Rice 1-deoxy-D-xyl	Non-reducing sacch	Nucleotide sequenc	M. tuberculosis re	M. tuberculosis an	Mycobacterium tube	M. tuberculosis im	Mycobacterium tube	. Myceliophthora the	Platenolide syntha	Platenolide syntha	Polyangium brachys	Pimaricin biosynth	S. venezuelae vep	cDNA sequence enco	Tripeptidyl aminop	S. lividans protea	S. aureofaciens DN	Total DNA sequence	Streptomyces roseo	Streptomyces freno	Mycobacterium tube	M. carbonacea DNA	M. tuberculosis re	M. tuberculosis an	Mycobacterium tube

ALIGNMENTS

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Matches 347
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18-NOV-1998;
28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1116
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                                                                                                                                                           ggcgctaccgggtgatcaaccaacgtatggggcgcgggagaccgcccagtgcattgaggtcg
ccgcctatccggccatctacttcgggtgccactggggcgcctgcacgagcaattcgggat
                                            ccggcaacggtttcgagatcacccaggccgacggttcggtgccgaccaacggcgccccga
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  98US-0104308
                                                   99WO-US11971
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1576..1715
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549..1564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides a cellulase from Actinomycetes. The cellula be used in a detergent composition, as an additive for animal feed for the treatment of textiles or pulp and paper. The DNA encoding cellulase can be used to identify homologous cellulases and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A novel Actinomocyes cellulase and related DNA, useful for compositions, treating textiles and paper or pulp \mbox{-}
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28-MAY-1999;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                            Transgenic
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tion, dental care
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/note= "fkbf
8156..8824
                   complement (11244..12092)
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complement (10987..11247)
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complement (9122..9883)
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complement (4595..5488)
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/note= "fkbJ gene"
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/note= "fkbR1 gene"
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Best Local S
Matches 149
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                                                                                                                                                                                                                                            05-NOV-1992;
06-NOV-1990;
12-NOV-1991;
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The invention concerns collagen-like polymers having repetitive triads with reduced proline content, and where glycine is the initial amino acid and the subsequent amino acids are varied. The choice of triads utilised in a recombinant collagen-like polymer are chosen in order to affect properties such as helix stability, hydration, solubility, gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27500
                                                                                                   Collagen-like polymers comprising repetitive triads - unicellular organisms with improved characteristics, uphotographic and medical fibres
                                                                                                                                                                                                                                                                                                                                                                                              collagen; repetitive triad motif; recombinant production;
photographic; medical; structural; fibre; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen-like
                                                                                                                                                                                                                                                                                              06-NOV-1990;
                                                                                                                                                                                                                                                                                                                      05-MAR-1996
                                                                                                                                                                                                                                                                                                                                              US5496712-A
                                                                                                                                                                                                                                                                                                                                                                                             photographic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT16766 standard; DNA;
                                                                             Example 2; Column 17-18; 43pp; English.
                                                                                                                                                                                                                    (PROT-) PROTEIN POLYMER.
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                                                                                                                                                       1996-150728/15.
DB; AAR93248.
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90US-0609716.
91US-0791960.
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useful in,
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Best Local Similarity
Matches 222; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              point, biodegradation and immunogenicity. Triads of particular interest include GAP, GPA, GPP, GAS, GPG, GPS, GAQ, GSP, GLQ, GPR, GAK, GAK, GAR, GER, GDR, GEP, GDA, GAH and GEA. The collagen-like polymers may impart new characteristics, finding wide used in photographic, medical, structural and fibre applications, and are capable of being produced in unicellular microorganisms at high mol. wts. and in high efficiency. Plasmid DNA from several colonies were analysed for inserts contg. multiple A6 DNA fragments by digestion with Fokl. The present sequence, was identified to contain the SequenceD gene 1 monomer sequence C2A24C2. The SequenceD collagen-like polymers are used as immunogens for the
                                               Triticum aestivum
                                                                            Wheat; 1-deoxy-D-xylulose 5-phosphate synthase; isoprenoid biosynthesis; herbicide; ss.
                                                                                                                         Wheat
                                                                                                                                                                                                                    AAA38763 standard;
                                                                                                                                                        14-SEP-2000
                                                                                                                                                                                       AAA38763;
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                                                                                                                        1-deoxy-D-xylulose
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ilarity 43.6%;
Conservative
                                                                                                                                                      (first entry)
Location/Qualifiers 31..1404
                                                                                                                                                                                                                    CDNA; 1404
                                                                                                                         5-phosphate synthase putative
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Best Local Similarity
Matches 220; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a putative coding sequence for the wheat 1-deoxy-D-xylulose 5-phosphate synthase enzyme (DXPS). Its protein is involved in the isoprenoid biosynthesis pathway. The cDNA was identified by sequencing a number of clones and then comparing their protein sequences to known proteins: this showed the sequence's similarity to the capsicum annuum DXPS sequence. The DXPS gene and protein can be used to create transgenic plants which express the gene at either different levels or at different stages of development compared to normal, and to identify herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 67; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide encoding 1-deoxy-D-xylulose 5-phosphate synthase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-DEC-1998;
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               cgcgtggccaccgtggaactggccggggccacctgggaagtctggtatgccgactgggac
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DB; AAY97425.
ccggcgccgccgtgggcgctcagcggcgcctcagcaagctgcagt 820
                                                                           gccatgacggccgggcaggcgtacgaggcgatgaacaacgccggctacctcgactcggac
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                                                                                                                                                            gccgtcgggagggacctcaagggcgcgaagaacaacgtggtggcggtgattggggacggg
                                                                                                                                                                                                                  gagtacgacagcttcggcaccggccacagctccaccatctccgccgccctcgggatg
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/product= "1-deoxy-D-xylulose 5-phosphate synthase"
/partial
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RESULT
ANA43032
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Best Local S
Matches 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAQ43030-34 encode examples of recombinantly produced DCP collagen-like polymers (CLPs) which consist of repeated tripeptide sequences selected from a wide range of GXY sequences, where X and Y can be any amino acid. These sequences can be cloned into plasmids and used to transform E. coli to produce the DCP proteins. DCP peptides comprise repeated units of; A = GAPGPAGPP, B = GSRGDPGPP and/or C = GAHGPAGPF. These polymers may be used to raise anti-DCP antibodies in rabbits. These polymers have molecular weights of >30 kD and are able to form helices due to interchain linkages. These polymers prof. contain a proportion of tripeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant; collagen-like polymer; CLP; tripeptide; helix; membrane; fibre; film; coating; triad sequence; collagen; mammalian; moulding; hydrogel; interchain linkage; colloid suspension; DCP; antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collagen-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High mol. wt. collagen-like protein polymers - capable of being
produced in unicellular microorganisms
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P-PSDB; AAR37738.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membranes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 triad sequences found in natural collagens, pref. mammalian collagens. The CLPs impart unique characteristics to materials such as fibres,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROT-) PROTEIN POLYMER TECHNOLOGIES
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gtgccactggggcgcctgcacgagcaattcgggattgccgcggcgcgtgcaggagctgtc
                                                       cacacgggccgatcacgacagcgaacaacgtggccgcctatccggccatctacttcgg
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymer DCP3-C2(AB12)C2 coding sequence
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Pred. No. 0.21
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                         This sequence encodes an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                            Tuberculosis; immunogenic; soluble; antigen; py vaccine; pharmaceutical; infection; diagnosis;
                                                                                                                                          Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - to develop products for the detection of M. tuberculosis infecti and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                    Campos-Neto A, E
Reed SG, Skeiky
                                                                                                                                                                                                                                                                                     13-MAR-1997;
11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                M. tuberculosis immunogenic polypeptide XP25 3'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV64548;
  Sequence 985
                                                                                                                  Claim 4; Page 176; 230pp; English.
                                                                                                                                                                                               WPI; 1998-261042/23
                                                                                                                                                                                                                                                                                                                           07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                   23-APR-1998
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                                                                                                                                                                                                                                                            (CORI-) CORIXA
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                                                                                                                                                                                                                                                                                                                                                                                                    tuberculosis.
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96US-0730510.
                                                                                                                                                                                                                      Dillon
y YAW,
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 138 A; 330 C;
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Twardzik DR,
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Vedvick TS;
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Query Match Best Local Similarity

6.2%;

Score Pred.

48.8; No. 0.

DB .24;

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Length

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                           Campos-Neto A, Dillo
Reed SG, Skeiky YAW,
                                                                                                                    07-OCT-1997;
                                                                                                                                                                                                                            Mycobacterium
                                                                                                                                                                                                                                                                                          AAV44439 standard; DNA; 985
          WPI; 1998-251292/22
                                                                                  13-MAR-1997;
11-OCT-1996;
                                                                                                                                         23-APR-1998.
                                                                                                                                                              WO9816645-A2
                                                                                                                                                                                  Mycobacterium
                                                                                                                                                                                                      Tuberculosis;
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                                                              (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                      infection; diagnosis; antigen; XP25;
                                                                                                                                                                                  tuberculosis strain
                                                                                                                                                                                                                            tuberculosis antigen
                                                                                  97US-0818111
96US-0729622
                                                                                                                    97WO-US18214
                                        Dillon
                              DC, Houghton
Twardzik DR,
                                                                                                                                                                                                                                                                                          ΒP
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                               R, Lodes MJ;
Vedvick TS;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the 3' region of DNA coding for an antigenic portion of Mycobacterium tuberculosis antigen xP25; 5' DNA is provided in AAV44438. XP25 DNA was isolated from a M. tuberculosis strain Erdman genomic DNA expression library using sera from patients having extrapulmonary tuberculosis. It bears no similarity to known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tuberculosis antigen, or an immunogenic portion of a M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transferted host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences. The invention relates to methods and compositions for diagnosing tuberculosis. It provides polypeptides (see AAW64391-W64379) comprising an antigenic portion of a soluble M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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develop products for the detection of M. tuberculosis infection
diagnosis of tuberculosis
  cacctgatcggcctagccgcacccgggaaagccgatccaacaggcgacgatgcc
                                                                                                                                             ctacgacatctggttcagtcccgtcacgaattccggcaacggctacagcggcggcggcga
                                                                                                                                                                                       9tccgacgtgcgcacgagctggacgctcacgccgatcacgacgggccgctggaatgccgc
                                                                                                                                                                                                                                  tgccactggggcgcctgcacgagc----aattcgggattgccgcgggcgcgtgcaggagct
                                                                                                                                                                                                                                                                           acacgggccgatcacgacaacggcaacaacgtggccgcctatccgggccatctacttcggg
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                                                                                                                                                                                                                                                                                                                                                                 cgtggaactggccggggccacctgggaagtctggtatgccgactgggactggaattacat
                                                                                      cggcaacggcgacggcgtcggcctgacagccaaggccggcgacggcggcgccgc
                                                                                                                                                                          gccgcaggtctcggcgacaacggcggggtcggcggtgacggtggggc-cggtggcgccgc
                                                                                                                                                                                                                    gccggcggccgcggtgacggcgatggggccagcggtctcggcctgggcctctcc
                                                                                                                                                                                                                                                                                                                                                    accggtaccggcgcccgcgttgtcggcgccaccggtagtgcaggcatcggcggg
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                                                                                                                                                                                                                                                                985
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                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; ilarity 44.9%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 138 A; 330 C;
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Pred. No. 0
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Matches 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAY39083 to AAY39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1998;
18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 985
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                          tgccactggggcgcctgcacgagc----aattcgggattgccgcgggcgcgtgcaggagct
                                                                                                                                                                                                                                                                              tgcggacgctgggacgcgcgatgttggccggggggcgctaccgggtgatcaacaacgta 183
ggctttgacggcggccaaggcggccaaggcggggccggcggcagcgccggccggccggc
                                                                                                        acacgggccgatcacgacaacggcaaccaacgtggccgcctatccgggccatctacttcggg
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                                                                                                                                                                                                            tggggcgcggagaccgcccagtgcattgaggtcggactggaaacgggcaacttcacgatc
                                                                                                                                                                                                                                                        accggtaccggcgcaccggcggcgttgtcggcgccaccggtagtgcaggcatcggcggg
                                                                                                                                                                                                                                                                                                                                          Page 171-172;
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SG, Sk
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98US-0025197
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YAW, Twardzik DR,
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Pred. No. 0
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ARESULT 12
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AC AAZ191
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                                          Query Match 6.3
Best Local Similarity 44.9
Matches 267; Conservative
                                                                                                                                                    This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as
                                                                                                                                                                                                                                                     Claim 4; Page 217; 323pp; English.
                                                                                                                                                                                                                                                                                                                                       Campos-Neto A,
Lodes MJ, Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. tuberculosis recombinant antigen DNA encoding 3'
                                                                                                               Sequence 985 BP;
                                                                                                                                                                                                                                                                                                             WPI; 1999-527416/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ19137 standard;
                                                                                                                                         current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                New polypeptide comprising antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-1999;
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R, Vedvick TS;
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                                                    /product=
                 complement
                            /*tag= f
                                                                                  /product- "ORF3" complement (3766..4276)
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/product= "ORF2"
complement (2683..3753)
                                                                                                                                                                 /*tag- b
1184..2767
                                                                                                                                                                                            /product= "ORF1"
complement (1069..1073)
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                                                           "ORF4"
                                                                                                   "ORF3"
                 (4526..5368)
                                            (4280..4284)
                                                                                                                                                                                                                                        (189..1064)
                                                                                                                                                                                                                                                                                                                                                   Everninomicin biosynthetic enzymes.
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combinatorial biosynthesis to generate libraries of orthomycins, e.g. everninomicin analogues/homologues and drug discovery. The DNA encoding the integrase allows for increasing a given gene dosage. The integrative vector can be used to permanently integrate copies of a heterologous gene of choice into-chromosomes of different hosts and to integrate genes which increase the yield of known products or to generate novel products such as hybrid antibiotics or other novel secondary metabolites. The vector can also be used to integrate antibiotic
                                                                                                                                                                                                                         useful for synthesising novel everninomicin-related compounds, arising from modifications of the DNA sequence designed to change glycosyl and modified orsellinic acid groups contained in everninomicin, for expressing functional or mutant everninomicin blosynthetic enzyme for evaluation, diagnosis and preferably biosynthesis of everninomicin or other secondary metabolic products, improving the yield of everninomicins and to produce novel everninomicins and also as a hybridisation probe to identify homologous sequences. The encoded polypeptides are useful for combinatorial biographics to control the product of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence encodes 11 proteins comprising enzymes of the everninomicin antibiotic biosynthetic pathway. A vector comprising a M. carbonacea everninomicin biosynthetic pathway resistance gene product is useful for selecting for a transfected or transformed host cell. An integrative version of the vector is useful for introducting a everninomicin pathway gene (a bottle-neck gene) into an actinomycete of the genus Micromonospora. The DNA encoding the biosynthetic proteins is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid molecules encoding everninomicin pathway gene products, useful for improving yields of everninomicin, to proverninomicin and as probes to identify homologous sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
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complement (6152..6156)
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complement (8141..8145)
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/product= "ORF10"
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                                                                                                                                                                                                                                                                            24-JUN-1998;
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Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ

Streptomyces sp

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CCC 1551 (AAI99683) and H37Rv (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                         Frenolicin; antibiotic; feed additive; anticoccidial; coccidiostatic; efflux pump; butyrate starter synthase; polyketide synthase; PKS; hemiketalase; ketoreductase; dehydrase; ketoreductase; hydroxylase; Streptomyces ros
                                                                                         Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly fro at seqdata.uspto.gov/sequence.html?DocID-6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189
                                                                                                                   11-MAY-1998
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9164..10012
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/note= "gene G (specifically claimed)"
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18895..19839
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                                                                                                                                                                                                                                                                                                                                                                                              in frenolicin synthesis. The genes can be divided into 5 subclusters: (1) genes A, B, C, D and F encode an efflux pump; (2) genes H, I, J and K encode butyrate starter synthases; (3) genes L, M and N encode polyketide synthases (PKS); (4) genes O, P, Q and R encode a hemiketalase, a ketoreductase and cyclases/dehydrases; and (5) genes S and T encode a keto/enoyl reductase and a hydrolase. Also claimed are vectors, host cells (especially a Streptomyces sp., particularly Streptomyces roseofulvus), and the encoded proteins. Cells transformed using the above sequence can be cultured to produce frenolicins or frenolicin precursors. The precursors can be converted to frenolicins by chemical or other methods. The frenolicins can be oxidised to frenolicin B, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sgo
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                                                                                                                                                                                                                                                                                                                                                                 antibiotic used as an anticoccidial agent. used as animal feed additives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 40-60; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces frenolicin gene cluster - useful for producing recombinant frenolicin antibiotics
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US/09104308 Tian E. Teij, Wilhelmus A.H. Teigen, Plet Talter No. 6187577el Cellulase Producing Cellulase Produced Therefrom and 1 3 3 Tr International, Inc. Title Titl	US-09-319-892-3 US-09-372-422A-9 US-08-584-226-3 US-07-642-734C-3 US-08-439-009A-3 US-09-443-501A-2 US-08-48-2-25-48 US-08-88-7-942C-7 US-08-913-264-2 US-08-913-264-2 US-08-913-264-2 US-08-859-586-4 US-09-385-028-13 US-09-103-840A-1
ng Actinomycetes, nd Method of Producing	Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 7, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli

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CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: PCT/US99/11971
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 09/104,308
PRIOR APPLICATION NUMBER: 09/974,042
PRIOR APPLICATION NUMBER: 08/974,042
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-19
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                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09321981 Patent No. 6287839
                                                                                                                                                                                                                         APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: No. 6287839el Cellulase Producing Actinomycetes,
TITLE OF INVENTION: Cellulase Produced Therefrom and Method of Producing
FILE REFERENCE: GC540-2
ORGANISM: Unknown FEATURE:
                              TYPE: DNA
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; OTHER INFORMATION: Nearest "neighbor" = ; OTHER INFORMATION: thermovebaceous US-09-321-981-2
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Best Local Similarity 50.7
Matches 347; Conservative
APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: No. 6287839el Cellulase Producing Actinomycetes,
TITLE OF INVENTION: Cellulase Produced Therefrom and Method of Producing
FILE REFERENCE: GC540-2
CURRENT APPLICATION NUMBER: US/09/321,981
CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: PCT/US99/11971
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 09/104,308
PRIOR APPLICATION NUMBER: 09/104,308
PRIOR APPLICATION NUMBER: 09/104,308
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Pred. No. 9.6e-21;
0; Mismatches 332;
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RESULT 4
US-08-642-255-50
; Sequence 50, Application US/08642255
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Best Local S
Matches 269
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SEQ ID NO 4
LENGTH: 1716
TYPE: DNA
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                                                                                                               APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              1185 aactcgttctcctccgcggtgaa 1207
COMPUTER READABLE FORM:
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                                                             ADDRESSEE: FLEHR, HOHBACH, TE:
STREET: 4 Embarcadero Center,
CITY: San Francisco
                              COUNTRY: USA
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Pred. No. 5.1e-15;
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; TOPOLOGY: lin
; MOLECULE TYPE:
; DESCRIPTION:
US-08-642-255-50
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Best Local Similarity 43.5%;
Matches 223; Conservative
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TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEFAX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 756 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303
                                    603 ctaccggcgcacgacgcccaccacgtcggtgag 635
                                                                                      638 CAGGCCCGCCAGGTGCGCCTGGACCGGCTGCTCCACCGGGTGCTCCGGGACCTGCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 atggggcgcggagaccgcccagtgcattgaggtcggactggaaacgggcaacttcacgat 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 gtgcggacgctgggacgcgcgcgatgtggccgggggggcgctaccgggtgatcaacaacgt 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: A55556-3/BIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                    gatgatctggctgaactggaacggcggcgtgatgccggggggcagccgcgtggccaccgt 542
                                                                                                                                                                                                                                                                                      cgacgtgcgcacgagctggacgctcacgccgatcacgacggcgctggaatgccgccta 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtgccactggggcgcctgcacgagcaattcgggattgccgcgggggggtgcaggagctgtc 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cacacgggccgatcacgacaacggcaacaacgtggccgcctatccggccatctacttccgg 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGACCGGCTGGTCCACCGGGTGCTCCGGGGACCTGCAGGCCCGCCAGGTGCGCCTGGAC
CGCCAGGTGCCCATGGCCCAGCAGGACCGAAAG
                                                                                                                         ggaactggccggggccacctgggaagtctggtatgccgactgggactggaattacatcgc 602
                                                                                                                                                                           GACCTGCAGGCCCAGGTGCGCCTGGACCGGCTGGTCCACCGGGTGCTCCGGGACCTG
                                                                                                                                                                                                                                                                CTCCGGGACCTGCAGGCCCGCCAGGTGCGCCTGGACCGGCTGGTCCACCGGGTGCTCCGG
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/desc = "synthetic"
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US-09-056-556-182
; Sequence 182, Application US/09056556
; Patent No. 6350456
; GENERAL INFORMATION:

RESULT

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US-09-056-556-182
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 18
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 985 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER: US,
FILING DATE: 07-APR-199
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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CITY: Seattle
STATE: Washing
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                    gctgatgatctggctgaactggaacggcggcgtgatgccggggcggcagccgcgtggccac 539
                                                                              ctacgacatctggttcagtcccgtcacgaattccggcaacggctacagcggcggcggcga 479
                                                                                                                                                                                             ATCANCGGGGCCGGGGGGCGGCGGCGACGGCGGCGCGCGCAACCGGT
                                                                                                                                                                                                                    acacgggccgatcacgacaacggcaacaacgtggccgcctatccggccatctacttcggg 303
GGGCAATGGCGGCAACGGGGGCCCGGCGGTGCTGGCGGGGCCGGCGACAACAATTTCAA 653
                                                                                                                             GCCGCAGGTCTCGGCGACAACGGCGGGGGTCGGCGGTGACGGTGGGGGC-CGGTGGCGCCGC
                                                                                                                                                          gtccgacgtgcgcacgagctggacgctcacgccgatcacgacgggccgctggaatgccgc 419
                                                                                                                                                                                                                                                            GCCGGCGCCGCCGCGTGACGGCGGCGATGGGGCCAGCGGTCTCGGCCCTGGGCCTCTCC
                                                                                                                                                                                                                                                                                                                                                        tggggcgcggagaccgcccagtgcattgaggtcggactggaaacgggcaacttcacgatc 243
                                                                                                                                                                                                                                                                                                                                                                                           ACCGGTACCGGCGCACCGGCGCGTTGTCGGCGCCACCGGTAGTGCAGGCATCGGCGGG
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Pred. No. 0.015;
0; Mismatches 322;
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APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DUA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ. ID NOS: 2
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US-09-103-840A-2/c
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent NO. 6294328
; GENERAL INFORMATION:
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Best Local Similarity
Matches 208; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3963722 GTCGGGTTCGGGAATACCGGCAACAACATCGGCACCGGAAACGCCGGCAGCGGCAAC 3963663
3963362 ACCGGTTTCGGGAACTCGGGTTCGCTCAACACGGGC 3963327
                                                                                                                                                                                                                                                                                                                                                                        3963602 ATCGGTTTCGGCAACACCGGCAACGGCAACATCGGCTTCGGGCTCACCGGCAACAACCAG 3963543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
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OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
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TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                               568 gtctggtatgccgactgggactggaattacatcgcc 603
                                                                                                                                                                                                              448 aattccggcaacggctacagcggcggcggcgagctgatgatctggctgaactggaacggc 507
                                                                                                                                                                                                                                                                                                  388 acgccgatcacgacgggccgctggaatgccgcctacgacatctggttcagtcccgtcacg 447
                                                                                                                                                                                                                                                                                                                                                                                                331 tcgggattgccgcggcgcgtgcaagg---agctgtccgacgtgcgcacgagctggacgctc 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 aacgtggccgcctatccgggccatctacttcgggtgccactggggggcctgcacgagcaat 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 gaggtcggactgggacacgggcaacttcacgatcacacgggccgatcacggacaacggcaac 270
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                                                                                                                                                                                    AACAACGTCGGTTTCTTCAACTCCGGCAACGGCAACCTGGGTATCGGCAACTCCAGCGAC 3963423
                                                                                                                                                                                                                                                                               GTGGGCATCGGTGGGCTGAACTCGGGCAGCGGAAACATCGGCTTGTTCAACTCGGGCACC 3963483
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Pred. No. 0.069;
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US-08-125-468-1/c
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                         24842
                                                                                                                                                                                                                                                                                                                                                                                         25022 GACCCGCAACGGCTTCGCCCTCGGCGAGGGGCGCGATGTTCGTGCTGGAGGAGCGGGA 24963
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  24728
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REFERENCE/DOCKET NUMBER: 31,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-Lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,468
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
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APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlortetracycline and tetracyline Formation and cosmids
                                                                                                                                                                                                                                                                           315
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                                                                                                                                                                               gagctggacgctcacgccgatcacgacgggccgctggaatgccgcctacgacatctggtt 434
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GGGCGACCACGCCTACCGGGTGCCGGTCAGCTCGATCAAGTCGATGATCGGACACTCGCT 24669
                        gaactggaacggcgtgatgccgggcggcagccgctggccaccgtggaactggccgg
                                                                                                          cagtcccgtcacgaattccggcaacggctacagcggcggcgcgagctgatgatctggct 494
                                                                                                                                                                                                                                  CAACTCCTACAGCATGACCGGGCTGCGGGGTCGACGGGAACGAGATGGCCGAGGCTATCCG 24843
                                                                         CGGCTCGGCGACCAA----GCAGAACGACCGGCACGAGACCGCCGCGTTCAAGAAGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253;
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Lotvin, Jason A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                ; TOPOLOGY: 11; MOLECULE TYPE: US-08-474-933-1
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                                                    Query Match
Best Local Similarity
Matches 253; Conserv
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                                                                                                                                                                                                                                                          TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 31,
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Strathy, Nancy APPLICANT: Fantini, Susan E.
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195 gaccgcccagtgcattgaggtcggactggaaacgggcaacttcacgatcacacgggccga 254
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Lotvin, Jason A.
Strathy, Nancy
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                                                        Conservative
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                                                                                                                                                                    DNA (genomic)
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                                                  Score 47.6; DB 2;
Pred. No. 0.044;
0; Mismatches 299;
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                                                                                        Length 30001;
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                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,508
FILING DATE: 23-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08173508 Patent No. 5616485
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 REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                  STREET: 3000 K Street, N.W. CITY: Washington, D.C.
                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner
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Best Local Similarity
Matches 185; Conserv
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
SEQUENCE 1908 base pairs
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Krieger, Timothy
Malek, Lawrence T.
Soostmeyer, Gisela
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Butler, Michael
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Pred. No. 0.038;
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Best Local
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Matches 185; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pairs
TYPE: nucleic acid
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FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/133/CACO
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APPLICATION NUMBER: US/01
FILING DATE: 24-JUN-1994
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                       551 ccggggccacctgggaagtctggtatgccgactgggactgg---aattacatcgcctacc 607
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TELEX: 904136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1,
                                                                                                                                                                                                                                                                                  TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/951,742 FILING DATE: 16-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                 FEATURE:
                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
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                                          NAME/KEY: misc_feature
LOCATION: 146..148
OTHER INFORMATION: /product= "Met at position -39
OTHER INFORMATION: represents fmet"
                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                     NAME: Bent, Stephen A. REGISTRATION NUMBER: 29 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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               NAME/KEY:
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146..1756
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sig_peptide
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US-09-105-537-1
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; ORGANISM: Streptomyces venezuelae
US-09-105-537-1
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                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA encoding methymycin FILE REFERENCE: 600, 438US1 CURRENT APPLICATION UNMEER: US/09/105,537A CURRENT FILING DATE: 1998-06-26 NUMBER OF SEQ ID NOS: 43 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1 1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09105537A Patent No. 6265202
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Best Local Similarity 46.7
Matches 185; Conservative
                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                            Matches
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   7706
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                  400 acgggccgctggaatgccgcctacgacatctggttcagtcccgtcacgaattccggcaac 459
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aaggacctgcggctcgacgccttcgtcctcttctcctccgtctccggcatcgtcggcacc
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                                                                                                                                                           Score 46.8; DB 4; Length 15872; Pred. No. 0.061;
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                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REGISTRATION NUMBER: 36,217
                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 887-0763
TRIEX: 706141
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 1288 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 2000 PENICITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20037
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                                       GTCRGSTTCGTGCGSTGCGACGTGTCSGTGGAGGASGACGTSSRGCGCGCCGTSGACTGS
                                                                     cyctaccygytyatcaacaacytatygygcycygagaccycccaytycattyagytcyga 219
                                                                                                                 GTGATCGCGGACATCGACGACGCSGCGGGSGAGGCGCTGGCGKCGGCGCTGGGSCCGCAS 398
                                                                                                                                                 gactgggactggaattacatcgcctacc-----ggcgcacgacgcccaccacgtcg 630
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ctggaaacgggcaacttcacgatcacacgggccgatcacgacaacggcaacaacgtggcc 279
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US-08-804-227C-7/c

: Sequence 7, Application US/08804227C

: Patent No. 5876991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Plant Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-1
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                             SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DeHoff, Bradley S. APPLICANT: Kuhstoss, Stuart P
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                                                                                                                                                                                                                                                                                                                                                                      ZIP: 46285
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/804, 227C
                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
    LENGTH:
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LILLY CORPORATE
44377 base pairs
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                                                                                                                                                                                                                                                                                                                                          Sequence 1, AFF----
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Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    18728 GGGACCGCCCTGCCCACCAGCAGGAGATGGCGCACCTTGTGCCGG
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                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
          CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                      APPLICANT: Richardson, Mark A. APPLICANT: Rosteck, Paul R., Jr. TITLE OF INVENTION: PLATENOLIDE
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                              CITY: INDIANAPOLIS
                                                                                                                                                                           STREET:
                                                                                                                                                                            ADDRESSEE: PAUL R. CANTRELL 1 STREET: LILLY CORPORATE CENTER
                                                                                                                               COUNTRY:
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gccgatcacgacaacggcaacaacgtggccgcctatccggccatctacttcgggtgccac 309
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                                                                                                                                                                                                                                                                                                                                                           Application US/08804198
                                                                                                                                 USA
                                                                                                                                                                                                                                                                                              Burgett, Stanley G. Kuhstoss, Stuart A.
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350..14002
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31329..36071
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20110..31284
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14046..20036
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            US/08/804,198
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Pred. No. 0.1;
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                                                                                                                                                                                                                                        SYNTHASE GENE
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Search completed: August 19, 2002, 13:45:36 Job time: 13940 sec
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ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION TAPORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.9%; Score 46; DB 2; Length 44377; Best Local Similarity 47.6%; Pred. No. 0.1; Matches 136; Conservative 0; Mismatches 150; Indels 0; Gaps
                                                                                                                                                                                                           18788 GGCGACCTCGGCACCCGACTCGGTCAACTCGGCGACCAGTCGACGCCGGGTGCGTC 18729
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LOCATION:
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NAME/KEY:
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36155..41830
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14046..20036
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350..14002
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31329..36071
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20110..31284
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Run
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                            0 0 0 0
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                                                                                                                                                                                                                     Score
    Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST:*
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Gapop 10.0 , Gapext 1.0
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786
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Copyright (c) 1993 - 2000 Compugen Ltd
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gb_est2:*
gb_htc:*
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em_estin: *
em_estmu: *
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em_gss_vrt:*
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12
                                                AU095988
2 AZ934730
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BE040131
2 AG060214
   AU030637
AV914669
BM373545
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                                                                        CNS010EW
BE517742
                                                                                                                                 CNS0091P
CNS0091P
CNS0072Q
BF253875
CNS003WG
AG060149
                                                                                                                                                                                                                                                         SUMMARIES
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AL053013 Drosophil
AL053013 Drosophil
AL065742 Drosophil
BF253875 HVSMEf000
AL065254 Drosophil
AG060149 Pan trog1
AL066051 Drosophil
BE040131 OD102C08
AG060214 Pan trog1
AL098882 Drosophil
BE047742 WHE0802_C
AU095988 AU095988
AZ934730 BJ_BA000
AZ934730 BJ_BA000
AU030637 AU030637
AV914669 AV914669
BM373545 EBma04_SQ
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FEATURES Source	REFERENCE AUTHORS TITLE JOURNAL COMMENT	S S Z	N C 1	44444 4 466666 7	118 4 19 19 4 4 20 19 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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melanogaster genome using these BACs. For further information please see http://www.fruiffly.org The BDGP Drosophila melanogaster BAC library was pripared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RRCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2: on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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BP 191 9100 EVEL CHOCK BY AND THE BEACH OF THE BOT OF T
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AL066742
AL066742.1 GI:4945205
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                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fi
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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47; Conservative
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Location/Qualifiers
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19116"
/note="end : TET3"
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                                                                                                                                                        BF253875 864 bp mRNA linear EST 22-OCT-2001
HVSMEf0002F20f Hordeum vulgare seedling root EST library HVcDNA0007
(Etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEf0002F20f, mRNA sequence.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Hordeum.
                                                                                                  BF253875.2 GI:13116780 EST.
                                                           Hordeum vulgare
                                                                                  barley.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14809"
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                             502 aacggcggcgtgatgccggggcggcagccgtggccaccgtggaactggccggggccacc 561
GACCTGGTGACGGAGCTGGACGCCAACTGGCCGACGCTGGCGTGCAAGGGGCGGGAAGAGC
                                                                                                         AGGAAGAAGTGCTGGCCGGAGTCCTGCAACAGCGAGCGCCTCAAGCTCTGGGAAATCAGG
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D.,
Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rwing@clemson.edu
Total hq bases = 333
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100 Jordan Hall, C
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On Nov 16, 2000 th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
260 c 271 g 161 t
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HVcDNA0007 (Etiolated and unstressed)"
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/lab_host="TJC121"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
aacggctacagcggcggcgcgagctgatgatctggctgaactggaacggcggcgtgatg
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                                                                     SGSTSTYBGCSVSGSSSTGSSGSSBGSRCCGSCTCBSSCSGCGSCCCSWKCGBTTTTSMS
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AL065254.1 GI:4942606
GSS.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR09E09"
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                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Telones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
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Pan troglodytes male lymphoblast DNA, clone_lib:PTB
BAC Library clone:PTB-047122.R.
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Pan troglodytes DNA, clone:
AG060149
AG060149.1 GI:16611379
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Totoki, Y., Watanabe, H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                         /cell_type="1ymphoblast"
/clone_lib="PTB Chimpanzee Male
291 c 334 g 15 t
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/db_xref="taxon:9598"
/clone="PTB-047I22.R"
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                                                                                                                                                                    /sex="male"
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Vatanabe,H. and Sakaki,Y.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
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Oryza sativa.
Oryza sativa
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and how to order individual BAC clones, the entire library,
filters for hybridization from the BACPAC Resource Center of
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Contact: Michalowski,C.B. University of Arizona
                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 1022)
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                                                             Scara, G., Wheeler, M. and Zepeda, Functional Genomics of Plant Str
                                                                                                       Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
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Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizo
An open reading fr
                                                                                                                                                            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                            Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AG060214

894 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-047K07.F, genomic survey sequence.
AG060214

AG060214.1 GI:16611446
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-047K07.F.
                                                                                                                                                                                                                                                                                                                                                        Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                    clone tracking errors.
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R.Site
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n reading frame exists.
1. .894
/organism="Pan troglodytes"
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/dev_stage="1 week"
/note="1 d 150mM NaC1"
285 c 292 g
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/strain="Pokkali"
/db_xref="taxon:4530"
/clone_lib="OD"
                                         Location/Qualifiers
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                                                        Drosophila melanogaster genome sur
BACN03P19 of DrosBAC library from
fly), genomic survey sequence.
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                            AL098882.1
fruit fly
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
a 380 c 398 g 7 t 26 others
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/clone="PTB-047K07.F"
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survey sequence SP6 end of BAC
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Drosophila melanogaster

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Triticum aestivum
Eukaryota; Viridiplantae;
                            bread wheat.
                                                           BE517742.1
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/note="end : SP6"
377 c 178 g
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                  GCCGGCCTCCGTCGACTCGTGGGTGGCCAACGCCGTGGCCTCGCTCTCGCGCCTCATCAA
                                                                                                                                                                                                                        agtctggtatgccgactgggactggaattacatcgcctaccggcgcacgacgcccaccac 626
                                                                                                                                                                                                                                                                           GAGCGTCATGGCCGGCCTCGGCGGCGACAGCGTGCTGGACATCGTCAAGGTCTCCTTCGC
                                                                                                                                                                                                                                                                                                        cggcgtgatgccggggcagccgcgtggccaccgtggaactggccgggggccacctggga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACGCCGGTGGCGCAGCAGCCCACGCCGGCGCCCACCAACGGCGTGTTCAGCGCGTTCTG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cacgccgatcacgacgggccgctggaatgccgcctacgacatctggttcagtcccgtcac 446
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                                             687
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1 (bases 1 to 449)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat
428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                800 Buchanan Street, Albany, Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Seeds were germinated and grown at 4 C for 5 weeks. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Five-week old seedling"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Wheat vernalized crown cDNA library"
/tissue_type="Crown tissue of seedling"
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                                                                                             TCGCCGACCCGTTCTGCCCGCGGANCCGCCGGC
                                                                                                              ccgtggaactggccggggccacctgggaagtctggtatgccgactgggactggaattaca
                                                                                                                                                                                                                                                                                          agctgattgatctggctgaactggaacggcggcggcgtgatgccgggggggcggcagccgcgtggcca
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                                                                                                                                                      TACAGATCTTGCTGTCCTTGTACGCCTTGGCGCCGTCGAAGCTCTCCGCGCCGTCGATCA
                                                                                                                                                                        ACGTGATCCCGGTCT----CCTCGTGGAATCTCCGGTGGAACTCCTGCATCGTCAGCATGT
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AU095988.1 GI
AU095988.1 GI
EST.
Oryza sativa.
Oryza sativa
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AU095988
   AZ934730
BJ__Ba0002F24r
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Rice cDNA from green shoot (2000)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.

1 (bases 1 to 682)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 81-298-38-7441
Fax: 81-298-38-7468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: tsasaki@abr.affrc.go.jp,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:4530"
/clone="S11827"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Rice green shoot"
/note="Green shoot (8 days old)"
184 c 212 g 132 t
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   4 bp
   library
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                                                                                                                                                                                                                                                                                                                                                                                           ggcgcctgcacgagcaattcgggattgccgcggcgcgtgcaggagctgtccgacgtgcgc
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BJ_Ba0003B10r B. japonicum genomic, DNA sequence.
AZ935386
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae Bradyrhizobium group; Bradyrhizobium.

1 (bases 1 to 546)
Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A., J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A. A marker-dense, sequence-ready map of the Bradyrhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bradyrhizobium japonicum.
Bradyrhizobium japonicum
Bacadyrhizobium japonicum
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Bradyrhizobium group; Bradyrhizobium.

1 (bases 1 to 534)
Tomkins J. P., Wood T.C., Stacey M.G., Loh, J.T., Judd, A.,
J.L., Stacey, G., Sadowsky, M.J. and Wing, R.A.
                                                                                          Bradyrhizobium japonicum.
Bradyrhizobium japonicum
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                                                                                                                                       AZ935386.1
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Class: BAC ends
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Fax: 864 656 4293
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100 Jordan Hall, Clemson,
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Location/Qualifiers
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/strain-"USDA110"
/db_xref-"taxon:375"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="B. Japonicum BAC library"
/lab_host="E. coli"
/lab_host="E. coli"
/note="Vector: pIndigo536; Site_1: HindIII"
/note="Vector: pIndigo536; Site_1: HindIII"
170 c 185 g 80 t
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TITLE
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Best Local Similarity
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                                                                                                                           1 (bases 1 to 644)
Sasaki,T. and Yamamoto,K.
Rice cDNA from immature leaf including apical munipublished (1997)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Nate Genome Research Program, Kannondai 2-1-2,
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Oryza sativa
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Location/Qualifiers
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Class: BAC ends
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Fax: 864 656 4293
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                                                                             305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
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100 Jordan Hall, Clemson,
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                                                tsasaki@abr.affrc.go.jp,
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/lab_host="E. coli"
/note="Vector: pIndigo536; Site_1: HindIII"
171 c 190 g 84 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bradyrhizobium japonicum"
/strain="USDA110"
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/organism="Oryza sativa"
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                                                              URL:http://rgp.dna.affrc.go.jp/
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                             659 tcgacgacgcggtcgcccgcggctacatccggc
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TCGCCGACCCGTTCTGCCCGCGGAGCCGCCGGC
                                                               TACAGATCTTGCTGTCCTTGTACGCCTTGGCGCNGTCGAAGCTCTCCGCGCCGCCGTCGATCA 47
                                                                                              tcgcctaccggcgcacgacgcccacgtcggtgagcgagctggacctgaaggccttca
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/db_xref="taxon:4530"
/clone="E60041_2z"
/clone_lib="Rice cDNA f
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/note="Organ: leaf; immature leaf including
meristem (under long day condition)"
meristem (under long day condition)"
163 c 197 g 127 t 7 others
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Search completed: August 19, Job time: 4372 sec 2002, 10:59:53

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Maximum Match 100%
Listing first 45 summaries
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AUTHORS
BASE COUNT
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Rhodothermus marinus
Bacteria; CFB group; Rhodothermus group; Rhodothermus.
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Sequence 3 from Patent WO0196382.
AX339682
                                                                                  Hreggvidsson,G.O.
Thermostable cellulase
Patent: WO 0196382-A 3 20-DEC-2001;
Prokaria ehf. (IS)
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                                                                                                                                                                                                                                  AX339682.1 GI:18135684
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            /organism="Rhodothermus marinus"
/db_xref="taxon:29549"
1 236 c 279 g 130 t
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Matches 732; Conservative 0;
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AX339680.1 GI:18
Wicher, K.B., Holst, O.P. Hreggvidsson, G.O. Thermostable cellulase Patent: WO 0196382-A 1
                               Rhodothermus marinus
Bacteria; CFB group; Rhodothermus
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                  Holst, O.P.,
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Pred. No. 4.7e-95;
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FIDDAVARGYIRPEWYLHAVETGFELWEGGAGLRSADFSVTVQ"
31 a 582 c 632 g 332 t
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Bacteria; CFB group; Rhodothermus
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Halldorsdottir,S., Thorolfsdottir,
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AF233376.1 G
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                                                                                                                                                                                                                                                                                                                                       Streptomyces sp. 11AG8.
Streptomyces sp. 11AG8
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                           Submitted (10-FEB-2000) Microbial & Molecular Screening, International B.V., Archimedesweg 30, 2333.CN Leiden, Th
                                                                                                                                                                                                  van Solingen,P., Meijer,D., van der Kleij,W.A.H.,
Bolle,R., Power,S.D. and Jones,B.E.
                                                                                                                                                Netherlands
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/note="Region:
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                     /gene="cell2A"
                                                  /gene="cel12A"
                                                                             /db_xref="taxon:133452"
                                                                                           /strain="11AG8
                                                                                                        /organism="Streptomyces
                                                                                                                                  Location/Qualifiers
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757. .792
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GCTTCGACGTCAAGGACTTCGTCGACCAGGCCGTCAGCCACGGCCTGGCCACCCCGGACT
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Jones, B.E., Van Der Kleij,W.A.H., Van Solingen,P. and Cellulase producing Actinomycetes cellulase produced method of producing same Patent: US 6187577-A 2 13-FEB-2001;
LOCATION/Qualifiers
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ccgactgggactggaattacatcgcctaccggcgcacgacgcccacgtcggtgagcg
                                                                                               c999c99ca9ccgcgtggccaccgtggaactggccgggggccacctgggaagtctggtatg
                                                                                                                              CCAACGGGGTGAACCGGACCGAGATCATGATCTGGTTCAACCGGGTCGGCCCGGTCCAGC
                                                                                                                                           acggctacagcggcggcgcgagctgatgatctggctgaactggaacggcgggggtgatgc
                                                                                                                                                                                                                                                                                                                                                                                    ctgagcccgagccgaccgtcgagctgtgcggacgctgggacgcgcgatgtggccgggg
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                                   GCAGCAACGGTTCGAACGACGTGATCTCCTTCCTGGCGCCCCTCCGCGATCAGCAGCTGGA
                                                                                   CCATCGCTTCGCCGGCACGCCCACGTCGGCGGCCGCAGCTGGGAGGTGTGGACCG
                                                                                                                                                                                                                           TGCCCATGCGGATCAGCTCGATCGGCAGCGCCCCAGCAGTGTCTCCTACCGCTACACCG
                                                                                                                                                                                                                                          tgccgcggcgcgtgcaggagctgtccgacgtgcgcacgagctggacgctcacgccgatca
                                                                                                                                                                                                                                                                         AGTCCTATCCCTCGGTCTACGACGGCTGCCACTACGGCAACTGCGCGCCCCGCACGACGC
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                                                                                                                                                                                                                                                                                                                                            gactggaaacgggcaacttcacgatcacagggccgatcacgacaacggcaacaacgtgg
                                                                                                                                                                                                                                                                                                                                                                      ACCGGTACGTGCAGAACAACCGCTGGGGCACCAGCGCCCCAGTGCATCAATGTGA
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Jones, B.E., Van Der Kleij, W.A.H., Van Solinge
Cellulase producing actinomycetes, cellulase
method of producing same
Patent: US 6287839-A 2 11.5EP-2001;
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Sequence 2 from
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432 c 340 g
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patent US 6287839
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Pred. No. 6.9e-10;
0; Mismatches 332;
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                                                                                                      tggacctgaaggccttcatcga-cgacgcggtcgccgcgggctacatccggccggagtgg 648
                                                                                                                                                                                                                                   AACTCGTTCTCCTCCGCGGTGAA
             gccgatttttccgtaacggtgca
                                               TACCTCACCAGCATCCAGGCGGGCTTCGAGCCGTTGGGAGGGCGGCACCGGTCTGGCCGTG
                                                                                           TCGACGTCAAGGACTTCGTCGACCAAGGCCGTCAGCCACGGCCTGGCCACCCCGGACTGG
                                                                                                                                         GCAACGGTTCGAACGACGTGATCTCCTTCCTGGCGCCCTCCGCGATCAGCAGCTGGAGCT 1064
                                                                                                                                                        TCGGTTCGCCGGTCGGCACGCCCACGTCGGCCGCCGCAGCTGGGAGGTGTGGACCGGCA
                                                                                                                                                                                                    gcggcagccgcgtggccaccgtggaactggccgggggccacctgggaagtctggtatgccg
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                                                                                                                                                                                                                                                                                                                                               cgcggcgcgtgcaggagctgtccgacgtgcgcacgagctggacgctcacgccgatcacga 349
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Sequence 4
AR168362
AR168362.1
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Jones, B.E., Van Der Kleij, W.A.H., Van Solingen, P. and Cellulase producing actinomycetes, cellulase produced method of producing same Patent: US 6287839-A 411-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown
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1. .1716
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611 c 559 g
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patent US 628
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6287839.
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304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces halstedii
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                  Similarity
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 Conservative
                                                                                                     TELGWDDLELIETVTNPPQTGSPGTDGGHYYWNLDLPSGRSGDAVMFIQWVRSDSOEN
FFSCSDVVFDGGNGEVTGIRGSGSTDDFTFTFTDFTFTDPHSGCMAVYRVTNYWS
GGFQGSVEVMNHSTTARDGMAVKWTPGAGAKVSSVWNGALTTGSDGAVTVRSLDYNRS
IPPDGSVTFGFTATSTGNNLPVGSIGCYNP"
1 1270 c 1106 g 528 t
                                                                                                                                                                                            YTNCSPGTNLPAQVSGIASAPSSISYGFVGSAVYNASYDIWLDPTPKKNGVNRTEIMI
WLNKVGPIQPIGSQAGTASVGGRTWQVWRGSNGSNDVISFVAPSAVASWSFDVMDFVR
NTIARGMAQNNWYLTSYQAGFEPWQNGAGLAVNSFSSTVNLGTPGTGSPGAPGEPVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Streptomyces
/strain="JM8"
/db_xref="taxon:1944"
595. .1728
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595. .1728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAC45429.1"
/db_xref="GI:2209260"
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                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                             /note="cellulose binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Cel2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="beta-1,4-endoglucanase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="celA2"
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Score 97.8; DI Pred. No. 3.3e 0; Mismatches
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Mastromei, G.
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Streptomyces rochei
Bacteria; Firmicutes;
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S.rochel eglS gene.
X73953
                                                                                    Mastromei,G.
Characterization and sequence
                                                                                                                   Perito, B., Hanhart, E., Irdani, T.,
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/organism="Streptomyces
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ggtatgccgactgggactggaattacatcgcctaccggcgcacgacgcccaccacgtcgg
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FGSTVIQGRYVVQNNRWGTSATQCVTATDSGFRVTQADGSVPTNGAPKSYPSVFNGCH
YTNCSPGTALPARISGISSAPSSISYGFVDNAVYNASYDIWLDPTPRTDGVNRTEIMI
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/db_xref="taxon:1928"
/clone="E.coli pCSF1"
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/protein_id="CAA52139.1"
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Characterization and sequence analysis of two genes involved cellulase degradation in Streptomyces viridosporus T7A, and i
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bactinomycetales; Streptomycineae; Streptomyces.
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DGVNRTTIMIWFNKVGPLQPIGSQVGTATVGGRTWQVWSGGNGSNDVLSFVAPSAIES
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                 /note="CelS1;
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Direct Submission
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Prairies, Laval, Quebec H7N 423, Canada
Sequence update by submitter
on Oct 2, 1997 this sequence version replaced
Location/Qualifiers
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Actinomycetales; Streptomycineae; Streptomyces.
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                                          CTGGTACCTGACGAGCGTTCAGGCGGGGTTCGAGCCGTGGCAGAACGGCGCCGGACTGGC
                                                            gtggtatctgcatgcggtggagacggggcttcgaactctgggagggcgggggcgggtctgcg
                                                                                                                                                                             tgccgactgggactggaattacatcgcctaccggcgcacgacgacgccacgtcggtgag
                                                                                                                                                                                                                                 9ccgggcggcagccgcgtggcaccgtggaactggccgggggccacctgggaagtctggta
                                                                                                                                                                                                                                                                                                                                               cacgacgggccgctggaatgccgcctacgacatctggttcagtcccgtcacgaattccgg
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                                                                                                                                                           CGGCGGCAACGGCTCGAACGACGTGCTGTCGTTCGTGGCACCGTCGGCGATCAGCGGCTG
                                                                                                                                                                                                                  GCCCATCGGCTCACCGGTGGGCACGGCCTCCGTCGGCGGCCGGACCTGGGAGGTGTGGAG
                                                                                                                                                                                                                                                                          CGACGGCGCCGTCTACAACGCCTCGTACGACATATGG-----CTGGACCCGACGGCCCG
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/function="hydrolase"
/product="cellulase B"
a 608 c 497 g 27
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IMIWFNRVGFIQPIGSPVGTASVGGRTWEVWSGGNSDVLLSFVAPSAISGNSEDVDD
EVRATVARGLAENDWYLISVQAGFEPWQNGAGLAVNSFSSTVETGTPGGTDPGDPGGP
SACAVSYGTNVWQDGFTADVTYTNTGTAPVDGWQLAFTLPSGQRTINAWNASLTPSSG
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448. .1470
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="celB"
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Pred. No. 0.0012;
0; Mismatches 324;
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MEDLINE
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          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                    The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted (23-NOV-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acyl-CoA dehydrogenase; aldehyde dehydrogenase; amidase; dihydroxy-acid dehydratase; DNA polymerase III beta chain; export protein; gntR-famly transcriptional regulator; lacI-famlly
                                                                                      jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If the cannot be identified we choose the most upstream initiation codon. If the possible in the insert of the sequence clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor sequencing at The Sanger Centre is funded
by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
3 (bases 1
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Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcriptional regulator; mark-family transcriptional regulator; oxidoreductase; reductase; regulatory protein; secreted cellulase precursor; secreted cellulose binding protein; tetk-family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (URL: http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oliver, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.nih.go.jp/
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                                                               G11A lies on the AseI-G genomic restriction fragment.
                                    Location/Qualifiers
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AVKAVRLPHDYLTERLIGEGTTDRGDVSGTGWMASGTERAYDEELLARVALDPALLPRV
VRPGEVAGTVBOGHGLPESKGTLVAACTGDINAAALGLGLRPGVPVMSLGTSGTAYAV
SQRRPADPTGTVAGFADARGDMLPLACTLICTLAVDRVASLLGLDREAVEPGTDYTLL
PFLDGETPNLPHSSGLLHGLRHDTTAGQLLQAAYGAVHSLLGALDLVUDADADPSA
PLLLIGGGARGTAWQOTVRRLSGRPVQI PEARELVALGAAAGAAGLLTGEDAAAVARR
PLLLIGGGARGTAWGOTVRRLSGRPVQI PEARELVALGAAAGAAGLLTGEDAAAVARR
WITAAGPYLDAVERDEATLIRITGVLSDAAPLLERDAASR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2StG11"
                                                                                                                                                                                           /translation="MSAPPHEAQPARPGRALPDTQQGMRRRNLSRYMHTVSAEGPLSR
AAVASRIGLTRAAVSTLVDELLRSGLLEELGPERFKVGRPGSALAVSGQPAGIGAE
VGVUPHLAVCAVDLRGRVRARAVXYGSURGRSPEPVLEGLTGLVRQVVSGAETEGLMGA
GLAVAVPGLVARDGRTVVRAPNLDWHDADLGALLPADLPPTVDNEANFGALAELWLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xylose repressor xylR, 384 aa; fasta scores: opt: z-score: 642.4 E(): 2.1e-28; 29.4% identity in 381 overlap. Contains match to Pfam entry PF00480 ROK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1525. .2733

'genee"SCG11A.02"

/notce="SCG11A.02"

/notce="SCG11A.02, possible xylose repressor, len: 402 aa;
similar to SW:XYLR_BACSU (EMBL:M27248) Bacillus subtilis
                                                                                                                           GTPRDFLHVSAEIGIGAAVVFDGRLLRGTRGFAGELGHVPVHPDGPRCACGGRGCLEQ
YAGEKAVLRAAGVEPGEDRVGLLAGRAAEGDEDVRRALREAGTALGIALTGAVNLLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250.
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/protein_id="CAB61582.1"
/db_xref="G1:6468422"
/translation="DPRQWWDALGEALSQCGEAAREAAAVSVGGQQHGLVTLDARGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Streptomyces coelicolor A3(2)"
/strain="A3(2)"
/db_xref-"taxon:100226"
                                                            DDPGAVAERA"
                                                                                                                                                                                                                                                                                                                         /product="putative xylose
/protein_id="CAB61583.1"
/db_xref="GI:6468423"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <1. .1299
/gene="SCG11A.02"
                                                                                                    EGVVLGGALAGLAPWLLPSLRDELARRTAGPACPVAVSELGPQGPLLGAAHSVVRAVL
                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SCG11A.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PS00445 FGGY family of carbohydrate kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="xylB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PS00933 FGGY family of carbohydrate kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="xylB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Pfam match to entry PF00370 FGGY, FGGY family of carbohydrate kinases, score 514.30, E-value 8.7e-151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene≖"xylB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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    .64 (+3.15 SD)"
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ggccgcctatccggccatctacttcgggtgccactggggcgcctgcacgagcaattcggg
                                                                                                                                                                                                                                                  GGGCAGGTACGTCCAGAACAACCGCTGGGGCTCCACCGCCACCCAGTGCGTCACGGC 27887
                                                                                                                                                                 cggactggaaacgggcaacttcacgatcacacgggccgatcacgacaacggcaacaacgt 224
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3041. 3646
/gene-"SCG11A.03"
/gene-"SCG11A.03"
/note-"SCG11A.03, probable amidase, len: 201 aa; similar /note-"SCG11A.03, probable amidase, len: 201 aa; similar to SW:AMPD_ECOLI (EMBL:X15237) Escherichia coli anhydro-N-acetylmuramy1-tripeptide amidase AmpD, 183aa; fasta scores: opt: 211 z-score: 267.1 E(): 1.7e-07: 39.5% identity in 114 aa overlap and to Streptonyces coelicolor SC2A11.21c; fasta scores: opt: 674 z-score: 751.6 E(): 0: 50.0% identity in 202 aa overlap. Contains match to Pfam entry PF01510 Amidase_2, N-acetylmuramoy1-L-alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative amidase"
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AYGIPKDRTHIIAHHEVPGSDHTDPGPFWDWTRYIRLVNFA"
3191. 3637
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SWRRS/KRGVGEPGTASVELMGGDLGAYRAFENETWELVRELLGTFRADGEHLLAV
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FIRRVQPWTCAAAPVHDPRTGRVLGAVDITGGDGLAHPHSLGFVQAVARAAESQLALL
TPERSASAAAETALGSADGRAVALSRPWELTMFVESDTSVVERRLRAGAVTAA
YEDGTVPPTLAAELARLGILGFDGLASAFVRLSRTWOFTWERTARGAVTAA
AAYAGPLLPGSQAPAYGRLRRRLADGLRAALIACGDPDLLADMAHAPWGEDDLDVWRA
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/gene="SCG11A.04"
/gene="SCG11A.04"
/note="SCG11A.04, possible transcriptional regulator, len:
aa; similar to TR:031551 (EMBL:Z99108) Bacillus subtilis
transcriptional regulator AcoR, 605 aa; fasta scores: opt:
393 z-score: 446.5 E(): 1.7e-17; 34.7% identity in 199 aa
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3821. .5080
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131.80, E-value 4e-38"
3041. .3646
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3821. .5080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative transcriptional regulator"
/protein_id="CAB61585.1"
/db_xref="GI:6468425"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAAVRPTAATSSRLAALESELAAPNPW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.0%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 324;
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No. 0.00047;
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Halobacterium sp. NRC-1 section
AE005123 AE004437
AE005123.1 GI:10581826
                                                                                              Ng,W.V., Kennedy,S.P., Mahairas,G.G., Berquist,B., Pan,M.,
Shukla,H.D., Lasky,S.R., Baliga,N., Thorsson,V., Sbrogna,J.,
Swartzell,S., Weir,D., Hall,J., Dahl,T.A., Welti,R., Goo,Y.A.,
Leithauser,B., Keller,K., Cruz,R., Danson,M.J., Hough,D.W.,
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Maddocks,D.G., Jablonski,P.E., Krebs,M.P., Angevine,C.M., Dale,H.,
Isenbarger,T.A., Peck,R.F., Pohlschrod,M., Spudich,J.L.,
Jung,K.-H., Alam,M., Freitas,T., Hou,S., Daniels,C.J., Dennis,P.P.
Omer,A.D., Ebhardt,H., Lowe,T.M., Liang,P., Riley,M., Hood,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                           Ng,W.V., Kennedy,S.P., Mahairas,G.G., Berquist,B., Pan,M.,
Shukla,H.D., Lasky,S.R., Baliga, N., Thorsson,V., Sbrogna,J.,
Swartzell,S., Weit,D., Hall,J., Dahl,T.A., Welti,R., Goov,Y.A.,
Leithauser,B., Keller,K., Cruz,R., Danson,M.J., Hough,D.W.,
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Jung,K.-H., Alam,M., Freitas,T., Hou,S., Daniels,C.J., Dennis,P.P.
Omer,A.D., Ebhardt,H., Lowe,T.M., Liang,P., Riley,M., Hood,L. and
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Halobacterium sp. NRC-1
Halobacterium sp. NRC-1
Archaes; Euryarchaeota; Halobacteria; Halobacteriales;
Submitted (14-JUL-2000) Institute for Roosevelt Way NE, Seattle, WA 98105, U
                                                    Direct Submission
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Proc. Natl. Acad. Sci. USA 97 (22), 12176-12181 (2000)
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of the
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FEATURES
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LITPDLERIADIAHNGVPLLVDNTFATPALATPIDHGADIVWHSTTKWIHGAGTTVG
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ATTTDAPVHAVDALEAY DDDRAHFWKMRKAGLP ILLSRTSDEHYPY EDTA IPADH
LPAFVADFQA ILDDLCTVASYY AHAGPGVLHV PRLVTLADEAGVAKMAE IADRVTDLV
LPAFVADFQA ILDDLCTVASYY AHAGPGVLHV PRLVTLADEAGVAKMAE IADRVTDLV
VEYGGAVSGEHGDGRARSQWNRK FYGEDLWAS FRRTKAAFDPDWI LNPG PVCGDAAGE
LDMTDHLRVA FDDFARAPLE PALNWDYENG FROMT ELCHGCAGCTGHQDTTGGCWRC PT
YRAANEETLSTRGRANMLRSANNGHLPADPLDDEFL FEVLDLCVGCKGCK ELCQC PSGVD
WASHLESTLSTRGRANMLRSANNGHLPADPLDDEFL FEVLDLCVGCKGCK ELCQC PSGVD
MAKLKTEVHIASHQADGVGVLDRLFGHTEALFHLGSALAPVSNWATALPGAGALAEKT
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SDAVMVQDDYHDLLSSAPAASVAANTYGVCEYLDRHGLDAAAGFDADGESLAYHGHCH
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SVLGGAIGNNSTGAHSLQYEKADGYLESAEVVLADGTVTTLGWVDTDDLDALADPDGD
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/transl_table=11
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                       complement(9890.
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VKHEGWNPTGSSKDROMFVGVRYAERLEVDRLACASTCORTSALLAAYGGRADTFVLL
LPAGKVAAGKIAQAALHGARICEVDGNEDDCLDVVAELAARGEAYLLNSLNPFRLEGQ
KTIAFELLEQSRTATGEWPDRLTVLPVGNAGNTAALYKAFRELVAAGAMTDDEMPALTG
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VQDRTTDAQRKLAGDGIGVEDASAASVAGLLALRERGEISADERVVCLTTGHLLKDPA
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aggtcggactggaaacgggcaacttcacgatcacacgggccgatcacgacaacggcaaca
                                                    ACACGGGCGCGAACAGCCACCCGTGATTCGTGCCCGCGATGCCCGCGCCGACGAGCG
                                                                                                                                          cggagcctgagcccgagccgtcgagctgtgcggacgctgggacgcgggcgatgtgg 100
                                                                      ccggggggcgctaccgggtgatcaacaacgtatggggcgcgggagaccgcccagtgcattg 160
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Steiner, B., Meyer, R., Bowen, M. and Morrill, W.
Random sequencing of Burkholderia pseudomalle1 strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steiner, B., Meyer, R., Bowen, M. and Morrill, W. Direct Submission
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                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                         SCGNPFVTARMODTAEGFGQPIREIFTPFFRIERQLPSPFDRQPAYRMSVADRTWHLL
YEPIAALANRVAALVGRLQTGRIAIYLTYSFIVLIALLTVVRRW"
1 1502 c 1477 g 538 t 1 others
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Pred. No. 0.41;
0; Mismatches
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Copyright (c) 1993 - 2000 Comp
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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48.8	49	49.4	49.8	53.6	57.6	131.6	131.8	131.8	Score	
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AAV64548	AAQ43032	AAA38763	AAT16766	AAA14651	AAA54513	AA257031	AAZ57029	AAV72359	ID	
M. tuberculosis im	Collagen-like poly	Wheat 1-deoxy-D-xy	Collagen-like poly	Nucleotide sequenc	Fructan exohydrola	DNA sequence of an	Actinomycetes cell	Actinomycete sp. 3	Description	

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44.4	44.6	44.6	44.6	44.6	44.6	44.6	44.6	44.6	44.6	44.8	44.8	44.8	45.2	45.2	45.2	45.2	45.2	45.2	45.6	46	46	46.8	46.8	47.2	47.2	47.2	47.6	47.6	47.8	47.8	48	48.4	48.8	48.8	48.8
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H. virescens inorg	Recombinant cosmid	Nucleotide sequenc	S. venezuelae pik	S. venezuelae pik	Sequence encoding	S. venezuelae macr	L05390 cDNA clone.	Polyangium brachys	Mouse Sox1 cDNA.	Non-reducing sacch	Rice 1-deoxy-D-xyl	Non-reducing sacch	Nucleotide sequenc	M. tuberculosis re	M. tuberculosis an	Mycobacterium tube	M. tuberculosis im	Mycobacterium tube	Myceliophthora the	Platenolide syntha	Platenolide syntha	Pimaricin biosynth	S. venezuelae vep	cDNA sequence enco	μ.		S. aureofaciens DN	Total DNA sequence	Streptomyces roseo	Streptomyces freno	Mycobacterium tube	M. carbonacea DNA	M. tuberculosis re	M. tuberculosis an	Mycobacterium tube

ALIGNMENTS

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ARZSULT AAV72359 ID AAVV XX AAV7 AC AAV7 XX ACTI DT 28-J DT 28-J XX Cell XX Cell XX M Pulf KW Ston KW Pulf KW mill XX ACTI XX ACTI XX MO99 PN WO99 PF 18-N XX 19-N PF 19-N XX 21-J PR 19-N XX 21-J PR 19-N XX J 24-JUN-1998; 19-NOV-1997; 19-NOV-1997; milling; ss Cellulase; detergent; animal feed; nutritional value; textile; stone washing; texture modification; appearance; cellulosic fabric; pulp; draining; papear; baking additive; starch treatment; grain; high fructose corn syrup production; ethanol production; fibre reduction; Jones BE, 27-MAY-1999. WO9925846-A2. Actinomyces sp. Actinomycete sp. 36kD cellulase DNA. 28-JUL-1999 AAV72359; AAV72359 standard; DNA; 1116 BP (GEMV) GENENCOR INT INC. 18-NOV-1998; Van Der Kleij WAH, (first entry) 98US-0104308. 97US-0974041. 97US-0974042. 98WO-US24649 Van Sollingen Ρ, Weyler W;

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Matches 347
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animal feeds and in treatment of textiles
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                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                  Claim 5; Fig 2; 72pp; English.
                                                                                                                                                                                                                                                                                              A novel Actinomocyes cellulase
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18-NOV-1998;
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       24-JUN-1998;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a cellulase from Actinomycetes. The cellulase of be used in a detergent composition, as an additive for animal feed and for the treatment of textiles or pulp and paper. The DNA encoding the cellulase can be used to identify homologous cellulases and for recombinant production of cellulases. The present sequence represents the DNA sequence of a complete expression cassette consisting of the promoter, celA signal sequence, cellulase 11AG8 and GI terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A novel Actinomocyes cellulase and related DNA, useful for detergent compositions, treating textiles and paper or \operatorname{pulp}
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ctgcatgcggtggagacgggcttcgaactctgggagggcgggggccggtctgcgaagcgcc
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99US-0321981.
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                                                                                                                                          Query Match
Best Local
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                                                                                                                                                                                                               Transgenic plants such as Cichorium intybus, Cynara scolymus, Helianthus tuberosus, Scorzonera hispanica, Oryza sativa, Zea mays, Triticum aestivum, Triticum durum, Hordeum vulgare, Secale cercale, Avena sativa, Socybum vulgare, Phleum pratense, Lolium temulentum, Dactylis glomerata, Pennisetum americanum, Allium cepa, Agave americanum, Agava azul teqilana, Sorghum bicolor and Panicum milaceum, transformed with a vector encoding a fructan exohydrolase (FEH) enzyme are useful for the recombinant production of FEH or other polypeptides having FEH activity. The FEH polypeptides produced are useful in detergents or as a detergent additive and in oral
                                                                                                                                                                                                                                                                                                                                                                  Novel DNA molecules encoding enzymes activity for use in transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA54513 standard;
                                                                                                                                                                                    Sequence 1983 BP; 357 A;
                                                                                                                                                                                                                                                                                                                                    Claim 9; Fig 4; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-007401/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fructan exohydrolase; FEH; transgenic plant; recombination; transgene; gene expression; detergent; detergen additive; oral care composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1187 tcgttctcctccgcggtgaa 1206
                                                                                                                                                                                                                                                                                                                                                         compositions, and in detergents
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (LEUV-) LEUVEN RES & DEV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-1999;
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               aacgtggccgcctatccggccatctacttcgggtgccactggggcgcctgcacgagcaat
   gacgtgcgcggctggctggactacg---gccacgtgtacgcgtccaagaccttc
                                                         gaggtcggactggaaacgggcaacttcacgatcacacgggccgatcacggacaacggcaac
                                                                                                  9cc999999cctacc9g9tgatcaacaacgtatg9g9cgcggagaccgcccagtgcatt 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gatttttccgtaacggtgca 731
                                           gtggggcggtacgacgcgggggacgcgttcgtgccggcggagcccgagcgcggggac~915
                                                                                    gccggggtgcggcacgtgctgaagctcagcgtgatggacacgctccaggaccactacatg
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No. 0.
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                                                                                                                                                                                                                                                                                                                                                                   hygroscopicus
                                                                                                                                        /*tag= f
/note= "fkbF
8156..8824
/*tag= ]
/note= "fkbJ gene"
complement (11244..12092)
                                           /note= "fkbI gene"
complement (10987..11247)
                                                                                                         /*tag= g
/note= "fkbG gene"
complement (9122..9883)
                                                                                                                                                                         6808..8052
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                                                                           complement (9894..10994)
                                                                                                                                                                                                         5601..6818
                                                                                                                                                                                                                                     complement (4595..5488)
                                                                                      /note= "fkbH
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/note= "fkbR1 gene"
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/note= "fkbV gene"
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tcgggattgccgcgcgcgcgcgcaggagctgtccgac-gtgcgcacgagctggacgctcac
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gtcgtcctgcaccgcggcacggcgctggccaccggaggcatgaacgagatcgtcggcg 1210
                                   ggcgtgatgccgggcgcgccgcgtggccaccgtggaactggccgggggccacctggg
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Streptomyces hygroscopicus var. ascomyceticus; immunophilin; FK-506 binding protein; polyketide compound; transplant rejectio graft-versus-host disease; uveitis; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; multiple sclerosis; primary biliary cirrhosis; scleroderma; neurite outgrowth; nerve regrowth; parkinson's disease; neurite outgrowth; nerve regrowth; parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of the FK-520 biosynthetic gene cluster.
traumatic spinal cord; brain injury;
                                                                                                                                                                                                                                                                 rejection;
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misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	CDS	misc_feature	misc_feature	FT misc_feature FT	misc_feature	misc_feature	misc_feature	FT misc_feature FT	misc_feature	misc_feature	misc_feature	FT misc_feature FT	FT CDS
/note= "ACP2" Complement (3382334480)	/note= "KS3" complement (3350533715) /*tag= ai	/note= "AT3" /note= "AT3" complement (3218533439) /*tag= ah	₹ .	/note= "KR3" (2986931018)	ad "ACP3" nent (29092	8750	ab "AT4" nent (27430	/"Lay da /nactive)" /note= "DH4 (inactive)" Complement (2614627430)	m .	ē ,	/ cuy /note= "KS5" complement (2399246573) /*tag= v	₽.	₩,	/note= "KR5" /complement (2024121420) /*tag= v	~ ~					/note= "compleme		compler /*tag=	ment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27680 GAAGTCCAACATCGGCCACACTCAGGCCGCCGCGGTGTCGCCGGTGTCATCAAGATGGT 27621
                                                                                                                                                                                                                                                              05-NOV-1992;
06-NOV-1990;
12-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27380
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The invention concerns collagen-like polymers having repetitive triads with reduced proline content, and where glycine is the initial amino acid and the subsequent amino acids are varied. The choice of triads utilised in a recombinant collagen-like polymer are chosen in order to affect properties such as helix stability, hydration, solubility, gel
                                                                                                                           Collagen-like polymers comprising repetitive triads unicellular organisms with improved characteristics, u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collagen-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT16766 standard;
                                                                                  Example 2; Column 17-18; 43pp; English.
                                                                                                               photographic and medical fibres
                                                                                                                                                                               WPI; 1996-150728/15.
                                                                                                                                                                                                          Cappello J,
                                                                                                                                                                                                                                                                                                                     06-NOV-1990;
                                                                                                                                                                                                                                                                                                                                               05-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                           collagen; repetitive triad motif; recombinant production; photographic; medical; structural; fibre; ds.
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                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                     (PROT-) PROTEIN POLYMER.
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nilarity 48.4%;
Conservative
                                                                                                                                                                                                           Ferrari FA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymer sequence D gene 2 encoding unit C2A24C2
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90US-0609716.
91US-0791960.
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Best Local Similarity
Matches 222; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         point, biodegradation and immunogenicity. Triads of particular interest include GAP, GPA, GPP, GAS, GPG, GPS, GAO, GSP, GLQ, GSP, GPK, GAK, GAR, GER, GER, GEP, GDA, GAH and GEA. The collagen-like polymers may impart new characteristics, finding wide used in photographic, medical, structural and fibre applications, and are capable of being produced in unicellular microorganisms at high mol. wts. and in high efficiency. Plasmid DNA from several colonies were analysed for inserts contg. multiple A6 DNA fragments by digestion with Fokl. The present sequence, was identified to contain the SequenceD gene 1 monomer sequence C2A24C2. The SequenceD collagen-like polymers are used as immunogens for the
CDS
                                               Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 756 BP; 82 A;
                                                                               Wheat; 1-deoxy-D-xylulose 5-phosphate synthase; isoprenoid biosynthesis; herbicide; ss.
                                                                                                                             Wheat 1-deoxy-D-xylulose 5-phosphate synthase putative coding sequence
                                                                                                                                                             14-SEP-2000
                                                                                                                                                                                            AAA38763;
                                                                                                                                                                                                                          AAA38763 standard;
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                                                                             isoprenoid
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                                                                            biosynthesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 67; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide encoding 1-deoxy-D-xylulose 5-phosphate synthase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
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P-PSDB; AAY97425.
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/product= "1-deoxy-D-xylulose 5-phosphate synthase"
/partial
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                                                                                                                                                                                                                 Query Match
Best Local S
Matches 223
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produced in unicellular microorganisms
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23; Conservative
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                                                                                                                                                  This sequence encodes an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
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                                                                                                    Sequence 985 BP;
                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - us to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1997;
11-OCT-1996;
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96US-0730510.
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6.78;
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Twardzik DR, Vedvick TS;
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Reed SG, Skeiky YAW,
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                                                                                                                                                                                Mycobacterium
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                                                                                                                                                                                                                          Mycobacterium tuberculosis antigen XP25 3'
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        WPI; 1998-251292/22
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11-OCT-1996;
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                                                                                                                                                                                                    infection; diagnosis; antigen;
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96US-0729622.
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                              DC, Houghton
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences. The invention relates to methods and compositions for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of a M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and crimers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis antigen XP25; 5' DNA is provided in AAV44438. XP25 DNA was isolated from a M. tuberculosis strain Erdman genomic DNA expression library using sera from partients having extrapulmonary tuberculosis. It bears no similarity to known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                            cggcggccagggtggtgccggccgggccaaggcggccagggcttgggggggaagcac
                                                                                                cgtggaactggccggggccacctgggaagtctggtatgccgactgggactggaattacat
                                                                                                                                 999caat99c9gcaac99999ccc9gc9gt9ct99cg9g9ccg9cgacaacaatttcaa
                                                                                                                                                                                                                                                                 gccgcaggtctcggcgacaacggcggggtcggcggtgacggtggggc-cggtggcgccgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region of DNA coding for an antigenic portion of tuberculosis antigen XP25; 5' DNA is provided in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48.8; DI Pred. No. 0.3; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G; 94 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                  548
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ID AAZ19349 RESULT 11

AAZ19349

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                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                    tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX39083 to
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                         AAY39225 are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 171-172; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-527409/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09942076-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ19349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunotherapy; diagnosis;
immune response; skin test
tuberculosis antigen 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigens from Mycobacterium tuberculosis useful in diagnostic n tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                       tgcggacgctgggacgcgcgatgtggccggggggggctaccgggtgatcaacaacgta 132
               tgccactggggcgcctgcacgagc----aattcgggattgccgcgggcgcgtgcaggagct
                                                                  acacgggccgatcacgacaacggcaacaacgtggccgcctatccggccatctacttcggg
                                                                                                                                                          accygtaccygcycaccygcyccyttytcygcyccaccygtaytycayycatcygcygy
                                                                                                                                                                                                             gccggcggccgcggtgacggcgatgggccagcggtctcggcctgggcctctcc
                                                                                                                                 tggggcgcggagaccgcccagtgcattgaggtcggactggaaaccgggcaacttcacgatc
                                                                                                                                                                                                                                                                  267;
                                                                                                                                                                                                                                                                                                                                 985 BP; 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0072967
98US-0025197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US03268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon DC, Hend
SG, Skeiky YAW,
                                                                                                                                                                                                                                                                             6.7%;
                                                                                                                                                                                                                                                                                                                                 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         test;
                                                                                                                                                                                                                                                                                                                                330 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XP25
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                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAW, Twardzik DR,
                                                                                                                                                                                                                                                                             Score 48.8;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                 423
                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence
                                                                                                                                                                                                                                                                                                                                 G; 94 T;
                                                                                                                                                                                                                                                                             .
W
                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                 322;
                                                                                                                                                                                                                                                                                                                                 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Houghton R; R, Vedvick
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                        Length
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234

192

252 354

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RESULT 12
AAZ19137
ID AAZ191
XX AAC19
CO AUC
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XX WYCOba
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                                                                            Query Match
Best Local S
Matches 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campos-Neto A, Dillon DC, Hendrickson RC, Ho Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen; vaccine;
                                                                                                                                                                                                  Sequence 985 BP; 138 A; 330 C; 423 G; 94 T; 0 other;
                                                                                                                                                                                                                                             nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel recombinant antigens and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-527416/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. tuberculosis recombinant antigen DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide comprising antigenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ19137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369
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                                                                          Local Similarity
nes 267; Conserv
  tttcccgatggcgacaacggaaacggaaccggagcctgagccgagccgaccgtcgagctg 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtccgacgtgcgcacgagctggacgctcacgccgatcacgacgggccgcttggaatgccgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 217; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis;
immunity; s
                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis.
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98US-0024753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection; infection; antibody; immunisation;
                                                                                                 6.7%;
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                                                                       Score 48.8; DB 20;
Pred. No. 0.3;
0; Mismatches 322;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houghton R; 
R, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
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                                                                          Indels
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                                                                          Gaps
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AAS08699/c
ID AAS086
     PRINTER TO THE PRINTER OF THE PRINTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS08699 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fermentation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; antibiotic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding Everninomicin biosynthetic enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carbonacea var. africana
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1184..2767
                       complement
                                              /*tag=
                                                                       complement
                                                                                                                                               /product= "ORF3"
complement (3766..4276)
                                                                                                                                                                                                                    /product= "ORF2" complement (2683..3753)
                                                                                                                                                                                                                                                                                                                                                 complement (1069..1073)
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                                                                                                      "ORF4"
                                                                                                                                                                        "ORF3"
                                                                                                                                                                                                                                                                                                                                                                             "ORF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bottle-neck
                         (4526..5368)
                                                                       (4280..4284)
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653 488

428 593

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everninomicin pathway gene (a bottle-neck gene) into an actinomycete of the genus Micromonospora. The DNA encoding the biosynthetic proteins is useful for synthesising novel everninomicin-related compounds, arising from modifications of the DNA sequence designed to change glycosyl and modified orsellinic acid groups contained in everninomicin, for expressing functional or mutant everninomic in biosynthetic enzyme for evaluation, diagnosis and preferably biosynthesis of everninomicin or other secondary metabolic products, improving the yield of everninomicins and to produce novel everninomicins and also as a hybridisation probe to identify homologous sequences. The encoded polypeptides are useful for combinatorial biosynthesis to generate libraries of orthomycins, e.g. everninomicin analogues/homologues and drug discovery. The DNA encoding the integrase allows for increasing a given gene dosage. The integrative vector can be used to permanently integrate copies of a possible of a contract of the contract of the product of the contract of t
                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence encodes 11 proteins comprising enzymes of the everninomicin antibiotic biosynthetic pathway. A vector comprising a M. carbonacea everninomicin biosynthetic pathway resistance gene product is useful for selecting for a transfected or transformed host cell. An integrative version of the vector is useful for introducing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecules encoding everninomicin pathway gene products, useful for improving yields of everninomicin, to proeverninomicin and as probes to identify homologous sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
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heterologous gene of choice into chromosomes of different hosts and to integrate genes which increase the yield of known products or to generate novel products such as hybrid antiblotics or other novel secondary metabolites. The vector can also be used to integrate antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 12; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAU04901, AAU04902, AAU04903, AAU04904, AAU04905, AAU04906,
AAU04907, AAU04908, AAU04909, AAU04910, AAU04911.
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complement (5392..6147)
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/product= "ORF10"
9568..9571
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Best Local
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 Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis; stran variation; epidemiology; patient
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                                                                                                                                                                             24-JUN-1998;
                                                                                                                                                                                                          24-JUN-1998;
                                                                                                                                                                                                                                                                         US6294328-B1
                                                                                                                                                                                                                                                                                                       Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI99683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI99683 standard; DNA; 4403765
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                                                                                                                                             (GENO-) INST
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                                                                                2001-647261/74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTGGACCTGGTCCCGCCCAACTACGCGGAGGTCTTCCGCTGCAACCTCCGGTCGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGACGCCAGTTTCCTGGCCGACGACGCGCAGCGGCTGGGCCCCCAGAACTGGGAAGGGCG
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                                                                                                                                             GENOMIC RES
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                                                                                                                                                                                                                                                                                                       tuberculosis
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                                                                                                                                                                                                          98US-0103840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  order to carry out bioconversions with compounds to normally sensitive and is thus useful in fermentation e.g. Streptomyces antibioticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.98;
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                            Frenolicin; antibiotic; feed additive; anticoccidial; coccidiostatic; efflux pump; butyrate starter synthase; polyketide synthase; PKS; hemiketalase; ketoreductase; dehydrase; ketoreductase; hydroxylaso.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen. Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and 137Rv (AAI99682). The method is useful for evaluating strain variation of the control of the sequences of M. tuberculosis and has valuable application in the fields of the control of the co
                                                                                                                Streptomyces
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/note= "gene J (specifically
complement (12154..13209)
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9164..10012
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Best Local Similarity
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P-PSDB; AAW34199-W34219.
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DATE: 19- TICON NUMBE DATE: 19- STAGENT INFO	08-2 2, Application US/09104308 1. 6187577 2, Application US/09104308 1. INFORMATION: 1NFORMATION: ANT: JONES, Brian E. ANT: Van Der Kleij, Wilhe ANT: Van Solingen, Piet ANT: Wyber, Walter OF INVENTION: No. 6187577 OF INVENTION: Cellulase P OF SEQUENCES: 25 Page Mill Road ET: 925 Page Mill Road ET: 925 Page Mill Road ET: California TRY: USA 94304-1013 ER READABLE FORM: ER READABLE FORM: ER READABLE FORM: BRIGHT SYSTEM: DOS WARE: FastSEQ for Windows TAPPLICATION DATA:	
E: 24 JUN-1998 E: 24 JUN-1998 ATION DATA: N NUMBER: 08/974, E: 19-NOV-1997 INT INFORMATION: ne, Christopher L. ON NUMBER: 35,696 DOCKET NUMBER: 35,696 DOCKET NUMBER: GC ATION INFORMATION: 650-845-6504 R SEQ ID NO: 2: RACTERISTICS: 116 base pairs leic acid SS: single linear	cation US/091043; 7 7 7 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8	1373 1333 599 20235 20235 1158 1158 71989 432 1155 1155 11894 11894 1182 1182 4403765 4411529
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                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/321,981
CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: PCT/US99/11971
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 09/104,308
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 08/974,042
                                                                                                                                                                                                                                                           APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: No. 6287839el Cellulase Producing Actinomycetes,
TITLE OF INVENTION: Cellulase Produced Therefrom and Method of Produ
FILE REFERENCE: GC540-2
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ORGANISM: Unknown FEATURE:
                                  TYPE: DNA
                                                  LENGTH: 1116
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US-09-321-981-4
; Sequence 4, Application US/09321981
; Patent No. 6287839
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                                                                                            GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: No. 6287839el Cellulase Producing
TITLE OF INVENTION: Cellulase Produced Therefrom and M
FILE REFERENCE: GC540-2
CURRENT APPLICATION NUMBER: US/09/321,981
CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: CT/US99/11971
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 09/104,308
PRIOR FILING DATE: 1998-06-24
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Pred. No. 2e-19;
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SEQ ID NO 4
LENGTH: 1716
TYPE: DNA
                                                                                                                                                                                                                                 Sequence 50, Application US/08642255 Patent No. 5773249
                                                                                               GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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Best Local Similarity
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COMPUTER READABLE FORM:
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                                                STREET: 4 Embarcade:
CITY: San Francisco
STATE: California
                               COUNTRY:
                                                                              ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & STREET: 4 Embarcadero Center, Suite 3400
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Pred. No. 5.1e-14;
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TELECOMMUNICATION INFORMATION:
TELLEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEO ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
Matches 223; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                   552 ctaccggcgcacgacgcccaccacgtcggtgag 584
                                                                         638 CAGGCCCGCCAGGTGCGCCTGGACCGGCTGCTCCACCGGGTGCTCCGGGACCTGCAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
CGCCAGGTGCCCATGGCCCAGCAGGACCGAAAG
                                                                                                             ggaactggccggggccacctgggaagtctggtatgccgactgggactggaattacatcgc 551
                                                                                                                                                                               gatgatctggctgaactggaacggcggcgtgatgccggggcggcagccgcgttggccaccgt 491
                                                                                                                                                                                                                                                        cgacatctggttcagtcccgtcacgaattccggcaacggctacagcggcggcgcgagct 431
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                                                                                                                                                                                                                                                                                                                                                                                                          gtgccactggggcgcctgcacgagcaattcgggattgccgcggggcgcgtgcaggagctgtc 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGACCGGCTGGTCCACCGGGTGCTCCGGGACCTGCAGGCCCGCCAGGTGCGCCTGGAC
                                                                                                                                                   GACCTGCAGGCCCGCCAGGTGCGCCTGGACCGGCTGGTCCACCGGGTGCTCCGGGACCTG
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US-09-056-556-182; Sequence 182, Application; Patent No. 6350456; GENERAL INFORMATION:

US/09056556

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NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Best Local :
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
 594
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                        13 tttcccgatggcgacaacggaaggaaccggagcctgagcccgagccgaccgtcgagctg 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 44.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                     gctgatgatctggctgaactggaacggcggcgtgatgccggggcggcagccgcgtggccac 488
                                                                                                                                                                                                                                                                                                                                                                                     tgcggacgctagggacgcgcgatgtggccgggggggcgctaccgggtgatcaacaacgta 132
GGGCAATGGCGGCAACGGGGGCGCCGGCGGCGGTGCTGGCGGGGGCCGGCGACAACAATTTCAA
                                                                            gtccgacgtgcgcacgagctggacgctcacgccgatcacgacgggccgctggaatgccgc 368
                                                                                                                                                                                 ATCAACGGGGCCGGGGGCGGCGGCAACGGCGACGGCGGGGACGGCGCAACCGGT
                                                                                                                                                                                                   tgccactggggcgcctgcacgagc----aattcgggattgccgcgggcgcgtgcaggagct 308
                                                                                                                                                                                                                                                             acacgggccgatcacgacaacggcaaccaacgtggccgcctatccggccatctacttcggg 252
                                                                                                                                                                                                                                                                                                     GCCGGCGGCGGCGGTGACGGCGGCGATGGGGCCAGCGGTCTCGGCCTGGGCCTCTCC
                                                                                                                                                                                                                                                                                                                                                               ACCGGTACCGGCGCACCGGCGCGTTGTCGGCGCCACCGGTAGTGCAGGCATCGGCGGG 294
                                                            CGGCAACGGCGGCAACGCGGCGTCGGCCTGACAGCCAAGGCCGGCGACGGCGGCGCCGC
                                                                                                                      GCCGCAGGTCTCGGCGACAACGGCGGGGGGTCGGCGGTGACGGTGGGGGC-CGGTGGCGCCGC
                                                                                                                                                                                                                                            tggggcgcggagaccgcccagtgcattgaggtcggactggaaacgggcaacttcacgatc 192
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
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LENGTH: 4403765
TYPE: DNA
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APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 208; Conserv
                                                                                                                                                                                                                                                                                 3963542 GTGGGCATCGGTGGGCTGAACTCGGGCAGCGGAAACATCGGCTTGTTCAACTCGGGCACC 3963483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3963662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3963722 GTCGGGTTCGGGAATACCGGCAACAACAACGTCGGCACCGGAAACGCCGGCAGCGGCAAC 3963663
3963362 ACCGGTTTCGGGAACTCGGGTTCGCTCAACACGGGC 3963327
                                                                                                                                                                                      3963482 AACAACGTCGGTTTCTTCAACTCCGGCAACGGCAACCTGGGTATCGGCAACTCCAGCGAC 3963423
                                                                                                                                                                                                                                                                                                                                                                          3963602 ATCGGTTTCGGCAACACCGGCAACGGCAACATCGGCTTCGGGCTCACCGGCAACAACCAG 3963543
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                            517 gtctggtatgccgactgggactggaattacatcgcc 552
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                                                                                        GCGAATGTGGGCATCGGAAACTCGGGGGCCACCGTGGGCCCGTTCGTGGCGGGCCATAAC 3963363
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45.6%;
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Pred. No. 0.088;
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Best Local Similarity
Matches 253; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (201)831-330:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Chi-
TITLE OF INVENTION: Chi-
TITLE OF INVENTION: Use
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      25022 GACCCGCAACGGCTTCGCCCTCGGCGAGGGCGCCGATGTTCGTGCTGGAGGAGCGGGA 24963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (20)831-2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle J
                                                                                                                                                                                                                                                                                                                                          204 tcacgacaacggcaacaacgtggccgcctatccggccatctacttcgggtgccactgggg
                                                                                                                                                                                                                                                                                                                                                                                                            144 gaccgcccagtgcattgaggtcggaactggaaacgggcaacttcacggatcacacgggccga 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 22-SEP-1993
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ZIP: 07470
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                                                                                                  cagtcccgtcacgaattccggcaacggctacagcggcggcgccgagctgatcggct 443
                                                                                                                                                                            cgcctgcacgagcaattcggggattgccgcggcgcgtgcaggagctgtccgacgtgcgcac 323
                                                                                                                                                                                                                                                                                                            GCACGCGATCCGGCGCGCGCGCACATCTACGCCGAGGTCACCGGCTACGCCGGGCGCTG
GGGCGACCACGCCTACCGGGTGCCGGTCAGCTCGATCAAGTCGATGATCGGACACTCGCT 24669
                                  gaactggaacggcggcgtgatgccgggcggcagccgcgtggccaccgtggaactggccgg 503
                                                                          CGGCTCGGCGACCAA---GCAGAACGACCGGCACGAGACCGCCGCGTTCAAGAAGAGCCCT
                                                                                                                                                    GGTC---GCGCTCGACCGCAGCCGGATGAACCCCCGAGGACGTCGGCTACGTCAACGCGCA 24786
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VENTION: Cloning of the biosynthetic pathway for VENTION: chlortetracycline and tetracyline Formation and cosmids
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Strathy, Nancy
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Query Match 6.5%;
Best Local Similarity 45.3%;
Matches 253; Conservative
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                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/125
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: TSEVOOS, ESTELLE J
REGISTRATION NUMBER: 31.145
REFERENCE/DOCKET NUMBER: 31.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
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                                                                                                                                                                                                           TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning
TITLE OF INVENTION: chlortet
TITLE OF INVENTION: useful t
NUMBER OF SEQUENCES: 1
                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 07470
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                                                                                                               DNA (genomic)
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Score 47.6; DB 2; pred. No. 0.076; 0; Mismatches 299;
                                   Length 30001
 Indels : 6;
Gaps
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144 gaccgcccagtgcattgaggtcggactggaaacgggcaacttcacgatcacacgggccga 203

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US-08-173-508-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1,
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APPLICANT:
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                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00
FILING DATE: 23-DEC-1993
CLASSIFICATION: 435
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                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                               ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jenish, David
APPLICANT: Krieger, Timothy
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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 ELECOMMUNICATION
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               REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                     T: 3000 K Street, N.W. Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08173508
                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bartfeld, Daniel
Butler, Michael J.
Hadary, Dany
                                                                                                                                                                                                                                                                                                        Foley & Lardner
INFORMATION:
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STREPTOMYCES
POLYPEPTIDES
                                                                                                                   US/08/173,508
                            29,768
                 18740/125/CACO
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                                                                                                                                                                                                                                                                                                                                                                         STRAINS FOR EXPRESSION OF PEPTIDES
                                                                                                                                                     Version
                                                                                                                                                     #1.25
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; LOCATION:
US-08-173-508-1
                                                                                                                                                             Sequence 1, Application US/08265310 Patent No. 5856166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                               APPLICANT:
                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: OTHER INFORMATION: FEATURE:
                                                                APPLICANT:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                             aactctgggagggcgggtctgcgaagcgccg 712
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                                                                                                                                                                                                                                                             CCGGCGGTCCCGGCGGCCTGCGTTTCCCGG
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                                                                                                                                               INFORMATION:
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Walczyk, Eva
Krygsman, Phyllis
                               Malek, Lawrence T. Soostmeyer, Gisela
                                                              Krieger, Timothy
                                                                               Jenish, David
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Pred. No. 0.076;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,310
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LENGTH: 1908 base pair
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
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LOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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REFERENCE/DOCKET NUMBER: 18
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CLASSIFICATION:
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CGGGCATCGACTGGGAGGACTGCGCAGCCGACTGGAACCTGCCCAAGCCCATCCAGTGCG
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23-DEC-1993
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STREPTOMYCES PROTEASES AND IMPROVED
STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES
POLYPEPTIDES
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Pred. No. 0.076;
0; Mismatches 208;
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                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pair
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                 FEATURE:
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                                            OTHER INFORMATION: /product= "Met at position -39 OTHER INFORMATION: represents fmet"
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TOPOLOGY: lir
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GENERAL INFORMATION:
APPLICANT: Sharman, D.H.
APPLICANT: Sharman, D.H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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; ORGANISM: Streptomyces venezuelae
US-09-105-537-1
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US-08-951-742-1
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Best Local Similarity 46.7
Matches 185; Conservative
                                                                                                                                                         Best Local Similarity Matches 172; Conserv
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                               LENGTH: 15872
                                                                               7646
                   349 acgggccgctggaatgccgcctacgacatctggttcagtcccgtcacgaattccggcaac 408
                                                                                                   289 ccgcggcgcgtgcaggagctgtccgacgtgcgcacgagctggacgctcacgccgatcacg 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 TOGCCGGCGCCGTCTCGGCACCCGCCGCGGAGCGCCCCGGCCGACGGCCACGGGCACG 278
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aaggacctgcggctcgacgccttcgtcctcttctcctccgtctccggcatcgtcggcacc
                                                                             cggctggacgcggtactgcgcccgaaggtcgacgccgcgtggaacctgcacgagctcacc 7705
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48.0%;
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                                                                                                                                                     Score 46.8; DB 4; Length 15872; Pred. No. 0.11; o; Mismatches 177; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 208;
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                                                                                                                                                                   Matches
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                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 706141
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A. 217
REGISTRATION UNMBER: 0546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEPHONE: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1288 base pairs
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DELLAPOR
TITLE OF INVENTION:
TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
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     169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2000 PEN CITY: WASHINGTON STATE: D.C.
                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
ZIP: 20037
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                                                       cgctaccgggtgatcaacaacgtatggggcgcggagaccgcccagtgcattgaggtcgga 168
                                                                                                         GTGATCGCGGACATCGACGCSGCGGGSGAGGCGCTGGCGKCGGCGCTGGGSCCGCAS 398
                                                                                                                           ctcaccccgctgcagggcctcgcgctcttcgacgccgcggtcgccagggacgacgccc
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ctggaaacgggcaacttcacgatcacacgggccgatcacgacaacggcaacaacgtggcc 228
                                   GTCRGSTTCGTGCGSTGCGACGTGTCSGTGGAGGASGACGTSSRGCGCGCCGTSGACTGS 458
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                                                                                                                                                                          Conservative
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                                                                                                                                                                                            6.3%; Score 46.2; DB 1; 38.5%; Pred. No. 0.12;
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MATERIALS AND METHODS FOR PRODUCING
PLANTS WITH SINGLE-SEX FLOWERS
                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05463-20001.00
                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2. E.
                                                                                                                                                                            346;
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                                                                                                                                                                                                            Length 1288;
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US-08-804-227C-7/c
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                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-2459 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                      COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DeHOFF, Bradley S. APPLICANT: Kuhstoss, Stuart A. APPLICANT: Rosteck, Paul R., Jr. APPLICANT: Sutton, Kimberly L. TITLE OF INVENTION: POLYKETIDE S.
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                     SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pai
                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: THOMAS G. PLANT 1501 STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tatctgcatgcggtggagacgggcttcgaactctgggagggcggggc 695
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nucleic acid
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IBM Compatible
SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                base pairs
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                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08804198 Patent No. 5945320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                              APPLICANT: Richardsou, Paul R., Jr.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                  18728
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                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
COMPUTER: Macintosh OPERATING SYSTEM: Macintosh SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/80
                                                                            ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Rao, Nagaraja R.
Richardson, Mark A.
Rosteck, Paul P
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US-08-804-198-1
Search completed: August 19, 2002, 14:01:35 Job time: 14899 sec
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ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: 99113
TELECOMMUNICATION: 11:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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is derived by analysis of the total score distribution.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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   AL053013 Drosophil
AL053013 Drosophil
AL066742 Drosophil
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AL065254 Drosophil
AG060149 Pan trogl
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AG060214 Pan trogl
AL068082 Drosophil
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ALIGNMENTS

REFERENCE AUTHORS TITLE RESULT 1 CNS0091P/c KEYWORDS SOURCE ACCESSION VERSION FEATURES COMMENT DEFINITION JOURNAL ORGANISM source melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm. Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. CNS0091P 925 bp
Drosophila melanogaster genome sur
BACR19D16 of RPCI-98 library from Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr Genoscope GSS. AL053013.1 Direct Submission fruit fly. (bases 1 to genomic survey sequence. /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_lib="RPCI-98" Location/Qualifiers GI:4934461 p DNA linear GSS 03-JUN-1999 survey sequence TET3 end of BAC # rom Drosophila melanogaster (fruit ø

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Best Local S
Matches 51
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TITLE
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPGI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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AL053013.1
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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/note="end : TET3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catctggttcagtcccgtcacgaattccggcaacggctacagcggcggcggcgagctgat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSWSAGGGSGSTGSTSSSSSSSSTSTSSSSVSSGSKSSTBSSGSBSSSGSSSSSSSSSSBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ccactggggcgcctgcacgagcaattcgggattgccgcgggcgcgtgcaggagctgtccga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acgggccgatcacgacaacggcaacaacgtggccgcctatccggccatctacttcgggtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKGCSSGSGBSCSCCSCSSSSSCSCCBCCCCCSCSSYCCSSSBSSSKCSSTSBSCSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gatctggctgaactggaacggcggcgtgatgccggggcagccgcgtggccaccgtgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCTSTSSSSSSSSSSTCSCCTCCCSYSYSSSTSSSSSTSWGSTSGSSSSSVGTSSSSDS
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

Www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                                                                                                                                                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 932)
                                                                                                                                                                                                                                                                                                                                                                                                                CNS0072Q 932 bp DNA LIHEGE GOVERN AND DESCRIPTION OF RPCI-98 library from Drosophila melanogaster (fruit BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                        Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                       fly), genomic survey sequence. AL066742
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/db_xref = "taxon: 7227"
/clone_libb "RPCI 98"
/clone="BACR19D16"
/note="end : TET3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctggacgctcacgccgatcacgacgggccgctggaatgccgcctacgacatctggttcag
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                                                                                                                                                                                                                                                                                                                                                  CS 931
                                                                                                                                                                                                                                                                                                                                                                                                                                      GSSCGGGSGCSSGCSSGGSGCCSSGSGGCCCSSGCGCGSCSSCGCGSGGCCSGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cacctgggaagtctggtatgccgactgggactggaattacatcgcctaccggcgcacgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSSSSGCGSGGCSSGCGSCGCGSCGSGCGSCGGSCGSSSGCGSSSGSGCGSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tcccgtcacgaattccggcaacggctacagcggcggcggccgagctgatgatctggctgaa 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STKGGSGGGGSBSBTKYTBKGKGGCGGSSGSCCSGGSCRGGGGGCGSCGCGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147;
                                                                                                                                                          UNG DE MRNA linear EST 22-OCT-2001 HVSMEf0002F20f Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0002F20f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Hordeum.
                                                                 Hordeum vulgare
                                                                                                                                 BF253875.2 GI:13116780
                                                                                                                                                                                                                                                                                                                                                                                           628
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/db_xref="taxon:7227"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14809"
/note="end : T7"
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                                                451 aacggcggcgtgatgccgggcggcagccgcgtggccaccgtggaactggccgggggccacc
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GACCTGGTGACGGAGCTGGACGCCAACTGGCCGACGCTGCCAAGGGCCGGGAAGAGC
                                                                                                            AGGAAGAAGTGCTGGCCGGAGTCCTGCAACAGCGCGCGCCTCAAGCTCTGGGAAATCAGG
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,R.D., Oates,R. and Main,D. 
Development of a genetically and physically anchored EST 
for barley genomics: Morex unstressed seedling root cDNA 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University
100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Total hq bases = 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Nov 16, 2000 this sequence version
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                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/gpages/bgn/31/cover.html) % a 260 c 271 g 161 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Hordeum vulgare seedling root EST library HVCDNA0007 (EtioLated and unstressed)" /tissue_type="Seedling root" /lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper
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Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegaw and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPGI-98 and was constructed by partial EcoRI digestion of Drosophila ban provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
  SGSTSTYBGCSVSGSSSTGSSGSSBGSRCCGSCTCBSSCSGCGSCCCSWKCGBTTTTSMS
                                                                                                          acgacgggccgctggaatgccgcctacgacatctggttcagtcccgtcacgaattccggc 405
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                                                                                                                                                             TTGCBSCSGCVYKTTTCBSCGGSGSTBYSCSSTSSCGSCCBYGSBGSGSBBGTSGKGSST 895
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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AL065254
AL065254.1 GI:4942606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                  Similarity 21.4
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/db_xref="taxon:7227"
/clone="hpCr-98"
/clone="BACR09E09"
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                                                                                                                                                                                                                                                                             Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                             (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Totoki,Y., Watanabe,H. ar
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-047122.R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/clone_lib="PTB Chimpanzee Male
291 c 334 g 15 t
                                                                           /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-047122.R"
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Determination of this BAC-end sequence was carried out as part of a Collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
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Drosophila melanogaster genome sur
BACR14N09 of RPCI-98 library from
Conomic survey sequence.
                                                                                                                                                                                                                                fruit fly.

Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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AL066051.1
                                                                                                                                                                     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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Bohnert,H.J., Borchert,C., Brazille,S., Brooks,
H., Kawasaki,S., McCollough,A., Michalowski,C.
Scara,G., Wheeler,M. and Zepeda,G.R.
Functional Genomics of Plant Stress Tolerance
                                                                                                                                                                                                                                                                   OD102C08 OD Oryza sativa cDNA transcription factors, mRNA se BE040131 BE040131.1 GI:8335147 EST.
Unpublished (2000)
Contact: Michalows
University of Ariz
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/clone="BACR14N09"
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Best Local
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Tel: 520-621-7992
Fax: 520-621-1697
Email: cbmdu.arizona.edu
An open reading frame exis
                                                                                                                                  Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes DNA, clone: PTB-047K07
AG060214
AG060214.1 GI:16611446
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-047K07.F.
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99; Conserv
                                                                                                                                                                                                                                                                         2 (bases 1 to 894)
Fujlyama,A., Hattor1,M., Toyoda,A., Taylor,T.D., Yada,
Totok1,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                          BAC
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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R.Site 2 : SacI.
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285 c 292 g
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/strain="Pokkali"
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                                                                          CNS010EW 1009 bp DNA linear GSS 26-JUL-19
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN03P19 of DrosBAC library from Drosophila melanogaster (fruit
Drosophila
                                                   fly), genomic
AL098882
          fruit fly
                                       AL098882.1
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/clone="PTB-047K07.F"
 melanogaster
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                                                               survey sequence.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Consular Part the bose and consular part the bose and consular part the bose and consular part that because the consular part that the bose and consular
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The structure and function of the expressed portigenomes - Vernalized crown cDNA library
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Sequence have been trimmed to remove vector
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Contact: Olin Anderson
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/tissue_type="Crown tissue of seedling"
/dev_stage="Five-week old seedling"
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/db_xref="taxon:4565"
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                                                                                                   TCGCCGACCCGTTCTGCCCGCGGANCCGCCGGC
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BJ__Ba0002F24r
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1. (bases 1 to 682)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2,
305-8602, Japan
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Oryza sativa
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AU095988
AU095988.1 GI:8858670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sasaki,T. and Yamamoto,K.
Rice cDNA from green shoot (2000)
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AU095988 Rice green shoot Oryza sativa cDNA clone S11827, mRNA
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/note="Green shoot (8 days old)"
184 c 212 g 132 t
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/strain="Nipponbare"
/db_xref="taxon:4530"
/clone="S11827"
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Pred. NO. 16;
0; Mismatches 205;
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Best Local Similarity
Matches 114; Conserv
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Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bacteria; proteobacteria; alpha subdivision; Rhizobiaceae
Bradyrhizobium group; Bradyrhizobium.
1 (bases 1 to 546)
Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A.,
,J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A.
,J.L., Stacey,G., sequence-ready map of the Bradyrhizobium
                                                                                                                                                                  genomic,
AZ935386
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Bradyrhizobium japonicum

Bardyrhizobium japonicum

Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae

Bradyrhizobium group; Bradyrhizobium.

1 (bases 1 to 534)
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Clemson University
100 Jordan Hall, Clemson, SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A., ,J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A. A marker-dense, sequence-ready map of the Bradyrhizobium
                                                                                                                                                                                               вл__ва0003в10г в.
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Location/Qualifiers
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                                                                                                                                                   AZ935386.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21376150
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/lab_host="E. coli"
/note="Vector: pIndigo536; Site_1: Hi
/note="Vector: pIndigo536; Site_1: Hi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Bradyrhizobium
/strain-"USDA110"
/db_xref-"taxon:375"
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Pred. No. 19;
0; Mismatches 108;
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                                                         305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp,
                                                                                                                                                                                1 (bases 1 to 644)
Sasaki,T. and Yamamoto,K.
Rice cDNA from immature leaf including
Unpublished (1997)
                                                                                                                                                                                                                                                   Oryza sativa.
Oryza sativa
Oryza sativa
Cryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U:
Tel: 864 656 7288
Fax: 864 656 4293
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21376150
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National Institute of Agrobiological Resources
National Research Program, Kannondai 2-1-2,
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Location/Qualifiers
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Class: BAC ends
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1. .644
/organism="Oryza sativa"
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/lab_host="E. coli"
/lab_host="E. coli"
/note="Vector: pindigo536; Site_1: HindIII"
/note="Vector: pindigo536; Site_1: dihers
171 c 190 g 84 t 1 others
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/strain="USDA110"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 546;
                                                                                                                                   Tsukuba,
                                                                                                                                                                                                                                                                                                                                                                                                                           EST 29-OCT-1998
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             368
                                                                                                                                                                                                                                                                                                                                                                                   343
                                                                                                                                                                                                                                                                                                                                                                                                                                                           403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 tcgggtgccactggggcgcctgcacgagcaattcgggattgccgcggcgcgtgcaggagc 307
                                 608 tcgacgacgcggtcgcccgcggctacatccggc 640
                                                                                                                                                   163
                                                                                                                                                                                                                           223 GCGGGATGTGCTCGCGGAACAAGCCCGTCGTCGCGATGCACCCCGGGTANAGCGACGCGA 164
                                                                                                                                                                                                                                                                                                                                                                                                       308 tgtccgacgtgcgcacgagctggacgctcacgccgatcacgacgggccgctggaatgccg 367
46
                                                                                                                                                                                                                                                           agctgatgatctggctgaactggaacggcggcgtgatgccggggcggcagccgcgtggcca 487
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TCGCCGACCCGTTCTGCCCGCGGAGCCGCCGGC
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                                                                                                         togectacoggegeacgacgeceaccacgteggtgagegagetggacetgaaggeettea 607
                                                                                                                                                   ACGTGATCCCGGTCT----CCTCGTGGAATCTCCGGTGGAACTCCTGCATCGTCAGCATGT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGCCTCCTGCGAGAGCTGGTTCTCGAACGACGCCGAGTCCTTGTTCCAGCTCCAGTACA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  מ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="immature"
/note="Organ: leaf; immature leaf including
meristem (under long day condition)"
meristem (under long day condition)
163 c 197 g 127 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            meristem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Nipponbare"
/db_xref="taxon:4530"
/clone="E60041_22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Rice cDNA from immature leaf including apical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49.2; D
Pred. No. 19;
0; Mismatches
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14
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